GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 8, 2005, 16:04:41 ; Search time 39 Seconds
(without alignments)
350.328 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHHHSSGIEGRMAPARS.....ENLKDFLLVIPFDCWEPVQE 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	673	88.0	144	1	FQHUGM	granulocyte-macrop
2	548	71.6	144	2	JH0469	granulocyte-macrop
3	544	71.1	144	1	A61632	granulocyte-macrop
4	480.5	62.8	143	1	FQBOGM	granulocyte-macrop
5	473	61.8	144	2	A44936	granulocyte-macrop
6	441	57.6	127	2	I46269	granulocyte-macrop
7	367.5	48.0	153	1	FQMSGM	granulocyte-macrop
8	84.5	11.0	2493	2	S72349	nonstructural poly
9	81	10.6	305	2	A56554	transcription fact
10	81	10.6	359	2	A55839	transcription fact
11	80.5	10.5	285	2	AH2390	tetrapyrrole methy
12	80.5	10.5	2493	2	S26372	nonstructural poly
13	79	10.3	610	2	A57632	homeotic protein B
14	78.5	10.3	329	2	T45972	hypothetical prote
15	78	10.2	496	2	S25091	cruciferin BnC2 -
16	78	10.2	816	2	S05548	gap protein hunchb
17	78	10.2	1019	2	T00117	dve protein - frui
18	77.5	10.1	420	2	T39712	hypothetical prote
19	77.5	10.1	427	2	T42516	hypothetical prote
20	75.5	9.9	292	2	I51171	transcription fact
21	75.5	9.9	942	2	JC2129	protein kinase PKN
22	75.5	9.9	1016	1	A46079	protein kinase C (
23	75	9.8	605	1	QQBE29	BRLF1 protein - hu
24	74.5	9.7	384	2	T41302	ferrochelatase pre
25	74.5	9.7	1305	2	T18548	flax rust resistan
26	73.5	9.6	248	2	T02647	probable MADS-box
27	73.5	9.6	1622	2	JE0378	DNA (cytosine-5-)-
28	73	9.5	234	2	T26429	hypothetical prote
29	73	9.5	461	2	S34472	MFH-1 protein - mo
30	73	9.5	943	2	T03306	PSD-95/SAP90-assoc
31	73	9.5	1183	2	A89135	protein F25G6.2 [i
32	73	9.5	1496	2	T00499	probable retroelem
33	72.5	9.5	289	2	D83709	hypothetical prote
34	72.5	9.5	417	2	C32185	Frz CD protein - M
35	72	9.4	311	2	G86383	probable mitochond
36	72	9.4	447	2	A34582	tryptophan 5-monoo
37	72	9.4	770	2	PN0105	RNA-directed RNA p
38	71.5	9.3	530	2	D70476	DNA helicase - Aqu
39	71.5	9.3	1273	2	T00338	hypothetical prote
40	71	9.3	398	1	TVFVVR	transforming prote
41	71	9.3	611	2	P82951	glutamine-fructose
42	70.5	9.2	265	2	T46089	proline-rich prote
43	70.5	9.2	601	1	B56564	transcription fact
44	70.5	9.2	633	1	A26030	serine/threonine-s
45	70.5	9.2	1025	2	H81751	exodeoxyribonuclea

ALIGNMENTS

RESULT 1
FQHUGM
granulocyte-macrophage colony-stimulating factor precursor [validated] - human
N;Alternate names: colony-stimulating factor 2; GM-CSF
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: C24636; I59065; A25169; A01853; A44175; JC1090
R;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
EMBO J. 4, 2561-2568, 1985
A;Title: Structure of the chromosomal gene for granulocyte-macrophage colony stimulating
A;Reference number: A91015; MUID:86030234; PMID:3876930
A;Accession: C24636
A;Molecule type: DNA
A;Residues: 1-144 <MIY>
A;Cross-references: UNIPROT:P04141; EMBL:X03021; NID:g31858; PIDN:CAA26822.1; PID:g31859
R;Kaushansky, K.; O'Hara, P.J.; Berkner, K.; Segal, G.M.; Hagen, F.S.; Adamson, J.W.
Proc. Natl. Acad. Sci. U.S.A. 83, 3101-3105, 1986
A;Title: Genomic cloning, characterization, and multilineage growth-promoting activity of
A;Reference number: I59065; MUID:86205844; PMID:3486413
A;Accession: I59065
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-144 <RES>
A;Cross-references: GB:M13207; NID:g181147; PIDN:AAA98768.1; PID:g181148
R;Cantrell, M.A.; Anderson, D.; Cerretti, D.P.; Price, V.; McKereghan, K.; Tushinski, R.
Proc. Natl. Acad. Sci. U.S.A. 82, 6250-6254, 1985
A;Title: Cloning, sequence, and expression of a human granulocyte/macrophage colony-stimu
A;Reference number: A25169; MUID:85298329; PMID:3898082
A;Accession: A25169
A;Molecule type: mRNA
A;Residues: 1-144 <CAN>
A;Cross-references: GB:M11734; NID:g181149; PIDN:AAA52122.1; PID:g181150
R;Lee, F.; Yokota, T.; Otsuka, T.; Gemmell, L.; Larson, N.; Luh, J.; Arai, K.; Rennick, I
Proc. Natl. Acad. Sci. U.S.A. 82, 4360-4364, 1985
A;Title: Isolation of cDNA for a human granulocyte-macrophage colony-stimulating factor
A;Reference number: A01853; MUID:85242684; PMID:3925454
A;Accession: A01853
A;Molecule type: mRNA
A;Residues: 1-144 <LEE>
A;Cross-references: GB:M11220; NID:g183363; PIDN:AAA52578.1; PID:g183364
R;Wong, G.G.; Witek, J.S.; Temple, P.A.; Wilkens, K.M.; Leary, A.C.; Luxenberg, D.P.; Jo
A.; Clark, S.C.
Science 228, 810-815, 1985
A;Title: Human GM-CSF: molecular cloning of the complementary DNA and purification of th
A;Reference number: A44175; MUID:85218749; PMID:3923623
A;Accession: A44175
A;Molecule type: mRNA
A;Residues: 1-116,'T',118-144 <WON>
A;Cross-references: GB:M10663; NID:g181145; PIDN:AAA52121.1; PID:g181146
A;Note: parts of this sequence, including the amino end of the mature protein, were conf
R;Wen, D.Y.; Huang, B.R.; Cai, L.W.; Si, J.Y.
Acta Biochim. Biophys. Sin. 25, 651-655, 1993

A;Title: Amplification of human granulocyte-macrophage colony-stimulating factor cDNA wi
A;Reference number: JC1090
A;Accession: JC1090
A;Molecule type: protein
A;Residues: 18-21,'C',23-96,'L',98-144 <WEN>
C;Genetics:
A;Gene: GDB:CSF2
A;Cross-references: GDB:119812; OMIM:138960
A;Map position: 5q23.2-5q31.1
A;Introns: 53/3; 67/3; 109/3
C;Function:
A;Description: stimulates the differentiation and proliferation of hematopoietic progeni
C;Superfamily: granulocyte-macrophage colony-stimulating factor
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status experimental
F;44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 88.0%; Score 673; DB 1; Length 144;
Best Local Similarity 100.0%; Pred. No. 2.8e-57;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 137

Qy        136 CWEPVQE 142
              |||||||
Db        138 CWEPVQE 144
```

RESULT 2
JH0469
granulocyte-macrophage colony-stimulating factor precursor - sheep
N;Alternate names: colony-stimulating factor 2; GM-CSF
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: JH0469; S16730
R;McInnes, C.J.; Haig, D.M.
Gene 105, 275-279, 1991
A;Title: Cloning and expression of a cDNA encoding ovine granulocyte-macrophage colony-s
A;Reference number: JH0469; MUID:92039044; PMID:1937025
A;Accession: JH0469
A;Molecule type: mRNA
A;Residues: 1-144 <MCI>
A;Cross-references: UNIPROT:P28773; GB:X53561; NID:g1800; PIDN:CAA37632.1; PID:g1801
C;Comment: This protein is a glycoprotein cytokine produced and secreted by various cell
C;Superfamily: granulocyte-macrophage colony-stimulating factor
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-144/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA
F;44/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 71.6%; Score 548; DB 2; Length 144;
Best Local Similarity 80.3%; Pred. No. 2.6e-45;
Matches 102; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

```
Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | ||| |:||:||:||:||  ||| | |||| |:|||||:||||| ||||||||||
Db         18 APTRQPSPVTRPWQHVDAIKEALSLLNDSTDTAAVMDETVEVVSEMFDSQEPTCLQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||||| | | |||||||||:||||| |||| ||||||:|||||||||| :||||
Db         78 LYKQGLRGSLTSLTGSLTMMASHYKKHCPPTQETSCETQIITFKSFKENLKDFLFIIPFD 137

Qy        136 CWEPVQE 142
              |||||||:
Db        138 CWEPVQK 144
```

RESULT 3
A61632
granulocyte-macrophage colony-stimulating factor precursor - sheep
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A61632
R;O'Brien, P.M.; Rothel, J.S.; Seow, H.F.; Wood, P.R.
Immunol. Cell Biol. 69, 51-55, 1991
A;Title: Cloning and sequencing of the cDNA for ovine granulocyte-macrophage colony-stimu
A;Reference number: A61632; MUID:91331592; PMID:1869289
A;Accession: A61632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-144 <OAB>
A;Cross-references: UNIPROT:Q9MYK4; GB:X55991; NID:g6983759; PIDN:CAA39463.1; PID:g698376
C;Superfamily: granulocyte-macrophage colony-stimulating factor
F;1-17/Domain: signal sequence #status predicted <SIG>

Query Match 71.1%; Score 544; DB 1; Length 144;
Best Local Similarity 79.5%; Pred. No. 6.4e-45;
Matches 101; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

```
Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | ||| |:||:||:||:||  ||| | |||| |:|||||:||||| ||||||||||
Db         18 APTRQPSPVTRPWQHVDAIKEALSLLNDSTDTAAVMDETVEVVSEMFDSQEPTCLQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||| | | |||||||||:||||| |||| ||||||:|||||||||| :||||
Db         78 LYKQGLRGSLTSLTGSLTMMASHYKKHCPPTQETSCETQIITFKSFKENLKDFLFIIPFD 137

Qy        136 CWEPVQE 142
              |||| |:
Db        138 CWEPAQK 144
```

RESULT 4
FQBOGM
granulocyte-macrophage colony-stimulating factor precursor - bovine
N;Alternate names: colony-stimulating factor 2; GM-CSF
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: JL0037
R;Maliszewski, C.R.; Schoenborn, M.A.; Cerretti, D.P.; Wignall, J.M.; Picha, K.S.; Cosmar
Mol. Immunol. 25, 843-850, 1988
A;Title: Bovine GM-CSF: molecular cloning and biological activity of the recombinant prot
A;Reference number: JL0037; MUID:89096971; PMID:3062386
A;Accession: JL0037
A;Molecule type: mRNA
A;Residues: 1-143 <MAL>
A;Cross-references: UNIPROT:P11052
C;Comment: This glycoprotein induces granulocyte, macrophage, and eosinophil colony forma
C;Superfamily: granulocyte-macrophage colony-stimulating factor
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-143/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA
F;44,54/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.8%; Score 480.5; DB 1; Length 143;
Best Local Similarity 68.5%; Pred. No. 7.6e-39;
Matches 87; Conservative 20; Mismatches 19; Indels 1; Gaps 1;

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Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | |: :|:||:||:||:||  ||| | || | ||:| ||:|| || ||||||||||:
Db         18 APTRPPNTATRPWQHVDAIKEALSLLNHSSDTDAVMNDT-EVVSEKFDSQEPTCLQTRLK 76

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||| ||:|||| | | |||||:||::|||||||||| || |:|::|||:||:|| :||||
Db         77 LYKNGLQGSLTSLMGSLTMMATHYEKHCPPTPETSCGTQFISFKNFKEDLKEFLFIIPFD 136

Qy        136 CWEPVQE 142
              |||| |:
Db        137 CWEPAQK 143
```

```
RESULT 5
A44936
granulocyte-macrophage colony-stimulating factor precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: A44936
R;Nash, R.A.; Schuening, F.; Appelbaum, F.; Hammond, W.P.; Boone, T.; Morris, C.F.; Slic
Blood 78, 930-937, 1991
A;Title: Molecular cloning and in vivo evaluation of canine granulocyte-macrophage colon
A;Reference number: A44936; MUID:91329842; PMID:1868252
A;Accession: A44936
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-144 <NAS>
A;Cross-references: UNIPROT:P48749; GB:S49738; NID:g233566; PIDN:AAB19466.1; PID:g233567
A;Note: sequence extracted from NCBI backbone (NCBIN:49738, NCBIP:49739)
C;Superfamily: granulocyte-macrophage colony-stimulating factor
F;1-17/Domain: signal sequence #status predicted <SIG>

  Query Match             61.8%;  Score 473;  DB 2;  Length 144;
  Best Local Similarity   68.5%;  Pred. No. 4e-38;
  Matches   87;  Conservative   19;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || |||:  |:| :||:|||||  ||| | |  | ||: |:|:||:|| : ||||:|||:
Db         18 APTRSPTLVTRPSQHVDAIQEALSLLNNSNDVTAVMNKAVKVVSEVFDPEGPTCLETRLQ 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||:||:|||| || ||||||:||||||||||: |||| | |:|||||||||  ||||
Db         78 LYKEGLQGSLTSLKNPLTMMANHYKQHCPPTPESPCATQNINFKSFKENLKDFLFNIPFD 137

Qy        136 CWEPVQE 142
              ||:||::
Db        138 CWKPVKK 144


RESULT 6
I46269
granulocyte-macrophage colony stimulating factor - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 09-Jul-2004
C;Accession: I46269
R;Smith, L.R.; Lundeen, K.A.; Diveley, J.P.; Carlo, D.J.; Brostoff, S.W.
Immunogenetics 39, 80, 1994
A;Title: Nucleotide sequence of the Lewis rat granulocyte-macrophage colony stimulating
A;Reference number: I46269; MUID:94041474; PMID:8225444
A;Accession: I46269
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-127 <SMI>
A;Cross-references: UNIPROT:P48750; EMBL:U00620; NID:g392779; PIDN:AAA18281.1; PID:g3927
C;Superfamily: granulocyte-macrophage colony-stimulating factor

  Query Match             57.6%;  Score 441;  DB 2;  Length 127;
  Best Local Similarity   63.0%;  Pred. No. 4e-35;
  Matches   80;  Conservative   19;  Mismatches   28;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || |||:| |:||:||:||:||  |||  |    | || |::||  | :| |||:||||:
Db          1 APTRSPNPVTRPWKHVDAIKEALSLLNDMRALENEKNEDVDIISNEFSIQRPTCVQTRLK 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||:|||| | |||:||||: :|||||| |  :: ||| | :||| ||  ||||
Db         61 LYKQGLRGNLTKLNGALTMIASHYQTNCPPTPETDCEIEVTTFEDFIKNLKGFLFDIPFD 120

Qy        136 CWEPVQE 142
              ||:|||:
Db        121 CWKPVQK 127


RESULT 7
FQMSGM
granulocyte-macrophage colony-stimulating factor precursor - mouse
N;Alternate names: colony-stimulating factor 2; GM-CSF; integral membrane protein
C;Species: Mus musculus (house mouse)
C;Date: 28-Aug-1985 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: I48368; I48369; A24636; A24645; A24644; A01854; A21882
R;Gough, N.M.; Metcalf, D.; Gough, J.; Grail, D.; Dunn, A.R.
EMBO J. 4, 645-653, 1985
A;Title: Structure and expression of the mRNA for murine granulocyte-macrophage colony st
A;Reference number: I48368; MUID:85230531; PMID:3874057
A;Accession: I48368
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-153 <RES>
A;Cross-references: UNIPROT:P01587; EMBL:X02333; NID:g51103; PIDN:CAA26192.1; PID:g51104
A;Accession: I48369
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 13-153 <RE2>
A;Cross-references: EMBL:X02333; NID:g51103; PIDN:CAA26193.1; PID:g51106
R;Miyatake, S.; Otsuka, T.; Yokota, T.; Lee, F.; Arai, K.
EMBO J. 4, 2561-2568, 1985
A;Title: Structure of the chromosomal gene for granulocyte-macrophage colony stimulating
A;Reference number: A91015; MUID:86030234; PMID:3876930
A;Accession: A24636
A;Molecule type: DNA; mRNA
A;Residues: 13-150,'G',152-153 <MIY>
A;Cross-references: GB:X03020; NID:g51098; PIDN:CAA26821.1; PID:g51099
A;Note: the sequence translated from the mRNA differs from that of the DNA in having 151-
R;Stanley, E.; Metcalf, D.; Sobieszczuk, P.; Gough, N.M.; Dunn, A.R.
EMBO J. 4, 2569-2573, 1985
A;Title: The structure and expression of the murine gene encoding granulocyte-macrophage
A;Reference number: A24645; MUID:86030235; PMID:3876931
A;Accession: A24645
A;Molecule type: DNA
A;Residues: 13-150,'G',152-153 <STA>
A;Cross-references: GB:X03020; NID:g51098; PIDN:CAA26821.1; PID:g51099
R;DeLamarter, J.F.; Mermod, J.J.; Liang, C.M.; Eliason, J.F.; Thatcher, D.R.
EMBO J. 4, 2575-2581, 1985
A;Reference number: A24644; MUID:86030236; PMID:3902470
A;Accession: A24644
A;Molecule type: mRNA
A;Residues: 13-153 <DEL>
A;Cross-references: GB:X03019; NID:g51100; PIDN:CAA26820.1; PID:g736260
R;Gough, N.M.; Gough, J.; Metcalf, D.; Kelso, A.; Grail, D.; Nicola, N.A.; Burgess, A.W.,
Nature 309, 763-767, 1984
A;Title: Molecular cloning of cDNA encoding a murine haematopoietic growth regulator, gra
A;Reference number: A01854; MUID:84245825; PMID:6610831
A;Accession: A01854
A;Molecule type: mRNA
A;Residues: 36,'I',38-150,'S',152-153 <GOU>
A;Cross-references: GB:X05906; NID:g51096; PIDN:CAA29336.1; PID:g51097
A;Experimental source: lung tissue
R;Sparrow, L.G.; Metcalf, D.; Hunkapiller, M.W.; Hood, L.E.; Burgess, A.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 292-296, 1985
A;Title: Purification and partial amino acid sequence of asialo murine granulocyte-macrop
A;Reference number: A21882; MUID:85113187; PMID:3871523
A;Accession: A21882
A;Molecule type: protein
A;Residues: 36,'I',38-69 <SPA>
C;Comment: It is unclear if Met-1 or Met-13 is the initiator.
C;Genetics:
A;Introns: 62/3; 76/3; 118/3
C;Superfamily: granulocyte-macrophage colony-stimulating factor
C;Keywords: cytokine; glycoprotein; growth factor; macrophage; monomer; T-cell
F;1-29/Domain: signal sequence #status predicted <SIG>
F;30-153/Product: granulocyte-macrophage colony-stimulating factor #status predicted <MA
F;95,104/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             48.0%;  Score 367.5;  DB 1;  Length 153;
  Best Local Similarity   54.3%;  Pred. No. 5.5e-28;
  Matches   69;  Conservative   23;  Mismatches   32;  Indels    3;  Gaps    1;
```

```
Qy          16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
               || |||   |:||:|| ||:||   |||  |    :|| |||:|  |  :: ||:||||:
Db          30 APTRSPITVTRPWKHVEAIKEA---LNLLDDMPVTLNEEVEVVSNEFSFKKLTCVQTRLK 86

Qy          76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
               :::|||||: ||||| | | ||:|: :|||||| | ||: |:  | ::|| ||  |||:
Db          87 IFEQGLRGNFTKLKGALNMTASYYQTYCPPTPETDCETQVTTYADFIDSLKTFLTDIPFE 146

Qy         136 CWEPVQE 142
               | :|||:
Db         147 CKKPVQK 153
```

RESULT 8
S72349
nonstructural polyprotein - eastern equine encephalomyelitis virus
N;Alternate names: nonstructural protein NSP1; nonstructural protein NSP2; nonstructural
C;Species: eastern equine encephalomyelitis virus
C;Date: 04-May-1998 #sequence_revision 15-May-1998 #text_change 09-Jul-2004
C;Accession: S72349
R;Weaver, S.C.; Hagenbaugh, A.; Bellew, L.A.; Netesov, S.V.; Volchkov, V.E.; Chang, G.J.
Virology 197, 375-390, 1993
A;Title: A comparison of the nucleotide sequences of eastern and western equine encephal
A;Reference number: S72349; MUID:94025587; PMID:8105605
A;Accession: S72349
A;Status: preliminary
A;Molecule type: genomic RNA
A;Residues: 1-2493 <WEA>
A;Cross-references: UNIPROT:Q88789; EMBL:U01034; NID:g393006; PIDN:AAC53734.1; PID:g3930
A;Note: readthrough of the terminator UGA occurs between the codons AAU for residue 1878
A;Note: the readthrough stopcodon UGA for residue 1879 is translated as X
C;Superfamily: Semliki Forest virus nonstructural protein

  Query Match   11.0%; Score 84.5; DB 2; Length 2493;
  Best Local Similarity 26.1%; Pred. No. 21;
  Matches   36; Conservative   17; Mismatches   54; Indels   31; Gaps   7;

```
Qy          17 PARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEV------------------- 57
               ||| |||   |    |       : :|  | :|  :   |:
Db        1678 PARIPSP---PCTSTNG--STTSIQSLGEDQSASASSGAEISVDHVSLWSIPSATGFDVR 1732

Qy          58 ISEMFDLQEPT--CLQTRLELY-KQGLRGSLTKLKGPLTMMASHYKQHC-PPTPETS--- 110
               |   |:||   :   |::  ||   |:  : |  | : |   |  | || |
Db        1733 TSSSLSLEQPTFPTMVVEAEIHASQGSLWSIPSITGSETRVPSPPSQDSRPSTPSASGSH 1792

Qy         111 CATQIITFESFKENLKDF 128
                :  :|||:|  | |:||
Db        1793 TSVDLITFDSVAEILEDF 1810
```

RESULT 9
A56554
transcription factor C/EBP - African clawed frog
N;Alternate names: CCAAT/enhancer core binding protein
C;Species: Xenopus laevis (African clawed frog)
C;Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: A56554
R;Xu, Q.; Tata, J.R.
Mech. Dev. 38, 69-81, 1992
A;Title: Characterization and developmental expression of Xenopus C/EBP gene.
A;Reference number: A56554; MUID:92399265; PMID:1525039
A;Accession: A56554
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305 <XU1>
A;Cross-references: UNIPROT:Q91346; GB:S44193; NID:g255566; PIDN:AAB23276.1; PID:g255567
A;Note: sequence extracted from NCBI backbone (NCBIN:113707, NCBIP:113708)
C;Superfamily: CCAAT/enhancer-binding protein alpha
C;Keywords: DNA binding; leucine zipper; transcription factor

  Query Match   10.6%; Score 81; DB 2; Length 305;
  Best Local Similarity 29.3%; Pred. No. 3.6;
  Matches   34; Conservative   17; Mismatches   35; Indels   30; Gaps   7;

```
Qy           2 HHHHHH--SSGIEGRMAPARSPSPS-------TQPWEHVNAIQ-EARRLLN-----LSRD 46
               ||||||  :| ::| ::|: | | |        :: |   |: :   ||  |       |||
Db         190 HHHHHHLQTSSLKG-ISPSSSTSSSSSESRGKSKKWVDKNSNEYRVRRERNNIAVRKSRD 248

Qy          47 TAAEMNETVEVISEMFDL-----------QEPTCLQTRLELYKQGLRGSLTKLKG 90
               |   |  ||   ::|:|            |    |:|   :::|    || |  |
Db         249 KAKMRN--VETQQKVFELSSDNDKLRKRVEQLSRELETLRGIFRQLPESSLVKAMG 302
```

RESULT 10
A55839
transcription factor inhibitor I-kappa-B-beta - mouse
C;Species: Mus musculus (house mouse)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55839
R;Thompson, J.E.; Phillips, R.J.; Erdjument-Bromage, H.; Tempst, P.; Ghosh, S.
Cell 80, 573-582, 1995
A;Title: IkappaB-beta regulates the persistent response in a biphasic activation of NF-ka
A;Reference number: A55839; MUID:95171452; PMID:7867065
A;Accession: A55839
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-359 <THO>
A;Cross-references: UNIPROT:Q8VC27; GB:U19799
C;Superfamily: unassigned ankyrin repeat proteins; ankyrin repeat homology; EGF homology
F;206-238/Domain: ankyrin repeat homology <AN3>

  Query Match   10.6%; Score 81; DB 2; Length 359;
  Best Local Similarity 20.0%; Pred. No. 4.4;
  Matches   28; Conservative   19; Mismatches   45; Indels   48; Gaps   4;

```
Qy           6 HHSSGIEGRMAPARSPSPSTQPWE-------------HVNAIQEARRLLNLSRDTAAEM 51
               |  : :: :  |      |  : |               ||  | :   :: | ||  |::
Db         174 HAPAAVDSQPNPENEEEPRDEDWRLQLEAENYDGHTPLHVAVIHKDAEMVRLLRDAGADL 233

Qy          52 NETVEVISEMFDLQEPTCLQTRLELYKQGLRGSLTKL---------------KGPL---- 92
               |:              |||| :| | |  :    |: :|               : ||
Db         234 NK-----------PEPTCGRTPLHLAVEAQAASVLELLLKAGADPTARMYGGRTPLGSAL 282

Qy          93 ----TMMASHYKQHCPPTPE 108
                   ::|   : |  | ||
Db         283 LRPNPILARLLRAHGAPEPE 302
```

RESULT 11
AH2390
tetrapyrrole methylase family protein [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AH2390
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anab
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-285 <KUR>
A;Cross-references: UNIPROT:Q8YN88; GB:BA000019; PIDN:BAB76379.1; PID:g17133817; GSPDB:GN
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: all4680
C;Superfamily: methyltransferase, YraL type

  Query Match   10.5%; Score 80.5; DB 2; Length 285;
  Best Local Similarity 23.8%; Pred. No. 3.7;
  Matches   29; Conservative   25; Mismatches   43; Indels   25; Gaps   5;

```
Qy          21 PSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL-ELYKQ 79
               |:   |  ||: |:|   | | :  ::   : ||:: ::|::       |   | :||::
```

```
Db        142 PAKGQQRREHLEALQTESRTL-IFYESPHRLRETLQDLAEVWGSDRQIVLARELTKLYEE 200

Qy         80 GLRGSLTKLKGPLTMMASHYKQHCP----------PTPETSCATQIITFESFKENLKDF 128
              |||: :         :||:|  |           |  ||     ::| |  |  |:
Db        201 FWRGSIGE-------AIAHYQQKEPQGEYTLLVAGNPPSET-----LLTEEQLKAELQQL 248

Qy        129 LL 130
              ::
Db        249 MM 250


RESULT 12
S26372
nonstructural polyprotein - eastern equine encephalomyelitis virus
N;Contains: nonstructural protein NSP1; nonstructural protein NSP2; nonstructural protei
C;Species: eastern equine encephalomyelitis virus
C;Date: 06-Jan-1994 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: S26369; S26372
R;Volchkov, V.E.; Volchkova, V.A.; Netesov, S.V.
Mol. Gen. Mikrobiol. Virusol. 5, 8-15, 1991
A;Title: Complete nucleotide sequence of the eastern equine encephalomyelitis virus genc
A;Reference number: S26369; MUID:91375524; PMID:1896061
A;Accession: S26369
A;Molecule type: genomic RNA
A;Residues: 1-2493 <VOL>
A;Cross-references: UNIPROT:Q66581; EMBL:X63135
A;Note: sequence could not be checked because of bad print in paper
A;Note: readthrough of the terminator UGA occurs between the codons AAU for residue 1878
A;Note: the readthrough stopcodon UGA for residue 1879 is translated as X
A;Accession: S26372
A;Molecule type: mRNA
A;Residues: 1886-2493 <VO2>
A;Cross-references: EMBL:X63135; NID:g59185; PIDN:CAA44847.1; PID:g1334981
A;Note: sequence could not be checked because of bad print in paper
A;Note: this reading frame extends between two stop codons and does not begin with a sta
C;Superfamily: Semliki Forest virus nonstructural protein
C;Keywords: nonstructural protein; polyprotein
F;1-532/Product: nonstructural protein NSP1 #status predicted <NS1>
F;533-1326/Product: nonstructural protein NSP2 #status predicted <NS2>
F;1327-1878/Product: nonstructural protein NSP3 #status predicted <NS3>
F;1886-2493/Product: nonstructural protein NSP4 #status predicted <NS4>

  Query Match             10.5%;  Score 80.5;  DB 2;  Length 2493;
  Best Local Similarity   27.8%;  Pred. No. 52;
  Matches   37;  Conservative   19;  Mismatches   56;  Indels   21;  Gaps    7;

Qy         17 PARSPS-PSTQPWEHVNAIQEARRLLNLSRDTAAEMN-ETVEV-----------ISEMF 62
              ||| || | |       :||      : |  : ||:: : | :           |
Db       1678 PARIPSPPCTSTNGSTTSIQSLGEYQSASASSGAEISVDQVSLWSIPSATGFDVRTSSSL 1737

Qy         63 DLQEPT--CLQTRLELY-KQGLRGSLTKLKGPLTMMASHYKQHC-PPTPETSCA---TQI 115
                |::||   :    |::  ||   |:  : |  | : |    |   | ||  | :    :
Db       1738 SLEQPTFPTMVVEAEIHASQGSLWSIPSITGFETRVPSPPSQDSRPSTPSASASHTFVDL 1797

Qy        116 ITFESFKENLKDF 128
              |||:|  | |:||
Db       1798 ITFDSVAEILEDF 1810


RESULT 13
A57632
homeotic protein BEL1 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 08-Feb-1996 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C;Accession: A57632
R;Reiser, L.; Modrusan, Z.; Margossian, L.; Samach, A.; Ohad, N.; Haughn, G.W.; Fischer,
Cell 83, 735-742, 1995
A;Title: The BELL1 gene encodes a homeodomain protein involved in pattern formation in t
A;Reference number: A57632; MUID:96097117; PMID:8521490
A;Accession: A57632
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-610 <REI>
A;Cross-references: UNIPROT:Q38897; GB:U39944; NID:g1122532; PIDN:AAB05099.1; PID:g112253
C;Genetics:
A;Gene: BEL1
C;Superfamily: unassigned homeobox proteins; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;391-450/Domain: homeobox homology <HOX>

  Query Match             10.3%;  Score 79;  DB 2;  Length 610;
  Best Local Similarity   22.7%;  Pred. No. 13;
  Matches   27;  Conservative   20;  Mismatches   42;  Indels   30;  Gaps    4;

Qy          2 HHHHHHSSGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNE------TV 55
              |||||| :             |  |   : :     | || |:: |  :|:|:
Db         72 HHHHHHQT-----------SGGTDQNQLLEDSSSAMRLCNVNNDFPSEVNDERPPQRPS 119

Qy         56 EVISEMFDLQEPTCL-----QTRLELYKQGLRG-------SLTKLKGPLTMMASHYKQH 102
              : :|       || :     : | :  :||  |       :|   :  : || ||:: :
Db        120 QGLSLSLSSSNPTSISLQSFELRPQQQQQQGYSGNKSTQHQNLQHTQMMMMMMNSHHQNN 178


RESULT 14
T45972
hypothetical protein F9D24.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C;Accession: T45972
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, January 2000
A;Reference number: Z23011
A;Accession: T45972
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-329 <DAN>
A;Cross-references: UNIPROT:Q9M2K4; EMBL:AL137081
A;Experimental source: cultivar Columbia; BAC clone F9D24
C;Genetics:
A;Map position: 3
A;Introns: 208/2; 238/3; 281/1
A;Note: F9D24.30

  Query Match             10.3%;  Score 78.5;  DB 2;  Length 329;
  Best Local Similarity   28.0%;  Pred. No. 6.8;
  Matches   21;  Conservative   12;  Mismatches   23;  Indels   19;  Gaps    3;

Qy          2 HHHHHHSSGIEGRMAPARSPSPSTQPWEHVNAIQE----------------ARRLLNLSR 45
              :||||||  | | : | || | :: | :| |:: :                  : | :
Db        106 NHHHHHS--INGNVGPTRSSSNTSTPSDH-NSLSDDDNNKEAPPSDHDHHMDNNVANQNN 162

Qy         46 DTAAEMNETVEVISE 60
                  ||: || |:
Db        163 AAGNNYNESDEVQSQ 177


RESULT 15
S25091
cruciferin BnC2 - rape
C;Species: Brassica napus (rape)
C;Date: 04-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 09-Jul-2004
C;Accession: S25091
R;Breen, J.P.; Crouch, M.L.
Plant Mol. Biol. 19, 1049-1055, 1992
A;Title: Molecular analysis of a cruciferin storage protein gene family of Brassica napus
A;Reference number: S25090; MUID:92379259; PMID:1511129
A;Accession: S25091
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-496 <BRE>
A;Cross-references: UNIPROT:P33524; EMBL:X59295; NID:g17791; PIDN:CAA41985.1; PID:g762920
C;Genetics:
A;Gene: BnC2
A;Introns: 95/1; 222/2; 362/3
C;Superfamily: glycinin
C;Keywords: seed; storage protein
```

Query Match 10.2%; Score 78; DB 2; Length 496;
Best Local Similarity 23.1%; Pred. No. 13;
Matches 27; Conservative 19; Mismatches 51; Indels 20; Gaps 3;

```
Qy          19 RSPS--------PSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCL 70
               |:||        |  | | |    |    :||          : ||::: | :   |
Db         219 RNPSQFYLAGKNPQGQSWLHGRGQQPQNNILN---------GFSPEVLAQAFKIDVRTAQ 269

Qy          71 QTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKD 127
               | :    :|  ||:: :::||  ::    |   |   | :   : |      :|| |
Db         270 QLQ---NQQDNRGNIVRVQGPFGVIRPPLKSQRPQETEANGLEETICSARCTDNLDD 323
```

Search completed: March 8, 2005, 16:14:10
Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 8, 2005, 15:56:25 ; Search time 177 Seconds
(without alignments)
410.821 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHHHSSGIEGRMAPARS.....ENLKDFLLVIPFDCWEPVQE 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	673	88.0	144	1	CSF2_HUMAN	P04141 homo sapien
2	664	86.8	144	2	Q647J8	Q647j8 homo sapien
3	653	85.4	144	2	Q9GL44	Q9gl44 macaca mula
4	633	82.7	144	2	Q865Y5	Q865y5 papio anubi
5	548	71.6	144	1	CSF2_SHEEP	P28773 ovis aries
6	544	71.1	144	2	Q9MYK4	Q9myk4 ovis aries
7	528	69.0	144	1	CSF2_CEREL	P51748 cervus elap
8	527	68.9	146	2	Q8WN17	Q8wn17 equus cabal
9	513	67.1	152	2	Q95L10	Q95l10 equus cabal
10	487	63.7	144	1	CSF2_PIG	Q29118 sus scrofa
11	486.5	63.6	143	2	Q6Q8A7	Q6q8a7 bubalus bub
12	480.5	62.8	143	1	CSF2_BOVIN	P11052 bos taurus
13	473	61.8	144	1	CSF2_CANFA	P48749 canis famil
14	472	61.7	141	2	Q7YRF7	Q7yrf7 felis silve
15	451	59.0	144	1	CSF2_FELCA	O62757 felis silve
16	441	57.6	127	1	CSF2_RAT	P48750 rattus norv
17	435.5	56.9	140	1	CSF2_CAVPO	Q60481 cavia porce
18	422.5	55.2	141	2	Q8VH40	Q8vh40 sigmodon hi
19	381.5	49.9	145	2	Q8CFB5	Q8cfb5 meriones un
20	361	47.2	138	2	Q99J91	Q99j91 marmota mon
21	360.5	47.1	141	1	CSF2_MOUSE	P01587 mus musculu
22	209.5	27.4	90	2	Q80XG1	Q80xg1 peromyscus
23	87	11.4	233	2	Q6ENY6	Q6eny6 oryza sativ
24	87	11.4	499	2	Q8IYK2	Q8iyk2 homo sapien
25	85	11.1	354	2	Q8NDL5	Q8ndl5 homo sapien
26	85	11.1	499	2	Q8N7T5	Q8n7t5 homo sapien
27	84.5	11.0	196	1	HUNB_DROAA	O46234 drosophila
28	84.5	11.0	2493	2	Q88789	Q88789 eastern equ
29	83	10.8	424	2	Q647M8	Q647m8 uncultured
30	83	10.8	785	2	Q8MQP8	Q8mqp8 drosophila
31	83	10.8	909	2	Q8THK7	Q8thk7 methanosarc
32	82.5	10.8	610	2	Q9CS72	Q9cs72 mus musculu
33	81.5	10.7	344	2	Q8RYL3	Q8ryl3 oryza sativ
34	81.5	10.7	965	2	Q8JZS5	Q8jzs5 rattus norv
35	81.5	10.7	1212	2	Q8K4T4	Q8k4t4 rattus norv
36	81	10.6	171	1	HUNB_SCAAL	O46254 scaptomyza
37	81	10.6	305	2	Q91346	Q91346 xenopus lae
38	81	10.6	343	2	Q9DG50	Q9dg50 xenopus lae
39	81	10.6	359	1	IKBB_MOUSE	Q60778 mus musculu
40	81	10.6	359	2	Q8VC27	Q8vc27 mus musculu
41	81	10.6	379	2	Q8SB73	Q8sb73 oryza sativ
42	81	10.6	379	2	Q7G6D7	Q7g6d7 oryza sativ
43	81	10.6	424	2	Q64E31	Q64e31 uncultured
44	80.5	10.5	285	2	Q8YN88	Q8yn88 anabaena sp
45	80.5	10.5	1371	2	Q7QRM3	Q7qrm3 giardia lam

ALIGNMENTS

RESULT 1
CSF2_HUMAN
ID CSF2_HUMAN STANDARD; PRT; 144 AA.
AC P04141; Q8NFI6;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE (Colony-stimulating factor) (CSF) (Sargramostim) (Molgramostin).
GN Name=CSF2; Synonyms=GMCSF;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85242684; PubMed=3925454;
RA Lee F., Yokota T., Otsuka T., Gemmell L., Larson N., Luh J.,
RA Arai K.-I., Rennick D.;
RT "Isolation of cDNA for a human granulocyte-macrophage colony-
RT stimulating factor by functional expression in mammalian cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4360-4364(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86205844; PubMed=3486413;
RA Kaushansky K., O'Hara P.J., Berkner K., Segal G.M., Hagen F.S.,
RA Adamson J.W.;
RT "Genomic cloning, characterization, and multilineage growth-promoting
RT activity of human granulocyte-macrophage colony-stimulating factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:3101-3105(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=85298329; PubMed=3898082;
RA Cantrell M.A., Anderson D., Cerretti D.P., Price V., McKereghan K.,
RA Tushinski R.J., Mochizuki D.Y., Larsen A., Grabstein K., Cosman D.;
RT "Cloning, sequence, and expression of a human granulocyte/macrophage
RT colony-stimulating factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6250-6254(1985).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=85218749; PubMed=3923623;
RA Wong G.G., Witek J.S., Temple P.A., Wilkens K.M., Leary A.C.,
RA Luxenberg D.P., Jones S.S., Brown E.L., Kay R.M., Orr E.C.,
RA Shoemaker C., Golde D.W., Kaufman R.J., Hewick R.M., Wang E.A.,
RA Clark S.C.;
RT "Human GM-CSF: molecular cloning of the complementary DNA and
RT purification of the natural and recombinant proteins.";
RL Science 228:810-815(1985).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=86030234; PubMed=3876930;
RA Miyatake S., Otsuka T., Yokota T., Lee F., Arai K.-I.;
RT "Structure of the chromosomal gene for granulocyte-macrophage colony
RT stimulating factor: comparison of the mouse and human genes.";

```
RL   EMBO J. 4:2561-2568(1985).
RN   [6]
RP   SEQUENCE FROM N.A.
RA   Kimmerly W., Bondoc M., Cheng J., Connolly K.S., Gunning K.M.,
RA   Davis C.A., Kadner K., Miguel T., Pitluck S., Pollard M., Rojeski H.,
RA   Subramanian S., Martin C.H.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A., AND VARIANTS ILE-115 AND THR-117.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [8]
RP   SEQUENCE OF 18-144 FROM N.A., AND VARIANT THR-117.
RC   TISSUE=Peripheral blood;
RA   Bhattacharya P., Pandey G., Mukherjee K.J.;
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
RN   [9]
RP   CARBOHYDRATE-LINKAGE SITES.
RX   MEDLINE=92144609; PubMed=1737041;
RA   Kaushansky K., Lopez J.A., Brown C.B.;
RT   "Role of carbohydrate modification in the production and secretion of
RT   human granulocyte macrophage colony-stimulating factor in genetically
RT   engineered and normal mesenchymal cells.";
RL   Biochemistry 31:1881-1886(1992).
RN   [10]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX   MEDLINE=92108420; PubMed=1837174;
RA   Diederichs K., Boone T., Karplus P.A.;
RT   "Novel fold and putative receptor binding site of granulocyte-
RT   macrophage colony-stimulating factor.";
RL   Science 254:1779-1782(1991).
RN   [11]
RP   X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX   MEDLINE=92235844; PubMed=1569568;
RA   Walter M.R., Cook W.J., Ealick S.E., Nagabhushan T.L., Trotta P.P.,
RA   Bugg C.E.;
RT   "Three-dimensional structure of recombinant human granulocyte-
RT   macrophage colony-stimulating factor.";
RL   J. Mol. Biol. 224:1075-1085(1992).
CC   -!- FUNCTION: Cytokine that stimulates the growth and differentiation
CC       of hematopoietic precursor cells from various lineages, including
CC       granulocytes, macrophages, eosinophils and erythrocytes.
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- POLYMORPHISM: Variant Ile-117 may be a risk factor for atopic
CC       asthma.
CC   -!- PHARMACEUTICAL: Available under the names Leukine (Immunex) and
CC       Leucomax (Novartis). Used in myeloid reconstitution following bone
CC       marrow transplant, bone marrow transplant engraftment failure or
CC       delay, mobilization and following transplantation of autologous
CC       peripheral blood progenitor cells, and following induction
CC       chemotherapy in older adults with acute myelogenous leukemia.
CC   -!- SIMILARITY: Belongs to the GM-CSF family.
CC   -!- DATABASE: NAME=Leukine; NOTE=Clinical information on Leukine;
CC       WWW="http://www.leukine.com/".
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M13207; AAA98768.1; -.
DR   EMBL; M11734; AAA52122.1; -.
DR   EMBL; M11220; AAA52578.1; -.
DR   EMBL; X03021; CAA26822.1; -.
DR   EMBL; M10663; AAA52121.1; -.
DR   EMBL; AC004511; AAC08707.1; -.
DR   EMBL; AF373868; AAK51563.1; -.
DR   EMBL; AF510855; AAM44054.1; -.
DR   PIR; C24636; FQHUGM.
DR   PDB; 1CSG; X-ray; A/B=18-144.
DR   PDB; 2GMF; X-ray; A/B=-.
DR   Genew; HGNC:2434; CSF2.
DR   MIM; 138960; -.
DR   GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; TAS.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
KW   3D-structure; Cytokine; Glycoprotein; Growth factor; Pharmaceutical;
KW   Polymorphism; Signal.
FT   SIGNAL       1    17
FT   CHAIN       18   144       Granulocyte-macrophage colony-stimulating
FT                              factor.
FT   DISULFID    71   113
FT   DISULFID   105   138
FT   CARBOHYD    22    22       O-linked.
FT   CARBOHYD    24    24       O-linked.
FT   CARBOHYD    26    26       O-linked.
FT   CARBOHYD    27    27       O-linked; partial.
FT   CARBOHYD    44    44       N-linked (GlcNAc. . .).
FT   CARBOHYD    54    54       N-linked (GlcNAc. . .).
FT   VARIANT    115   115       T -> I (in dbSNP:2069640).
FT                              /FTId=VAR_013089.
FT   VARIANT    117   117       I -> T (in dbSNP:25882).
FT                              /FTId=VAR_001975.
FT   CONFLICT    96    96       M -> K (in Ref. 8).
FT   CONFLICT   123   123       F -> L (in Ref. 8).
FT   TURN         25    27
FT   HELIX        30    45
FT   HELIX        50    53
FT   TURN         54    54
FT   STRAND       56    60
FT   TURN         66    67
FT   HELIX        72    81
FT   TURN         82    82
FT   HELIX        85    90
FT   HELIX        91   104
FT   STRAND      115   119
FT   HELIX       120   131
FT   TURN        132   133
SQ   SEQUENCE   144 AA;  16295 MW;  75D1E50506BCA7A8 CRC64;

  Query Match           88.0%;  Score 673;  DB 1;  Length 144;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-54;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 137

Qy        136 CWEPVQE 142
              |||||||
Db        138 CWEPVQE 144


RESULT 2
Q647J8
ID   Q647J8      PRELIMINARY;      PRT;   144 AA.
AC   Q647J8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
```

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DE   Granulocyte-macrophage colony stimulating factor 2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Li C.;
RL   Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY720441; AAU21240.1; -.
SQ   SEQUENCE   144 AA;  16269 MW;  75D1E0B9D4D1A1A8 CRC64;

  Query Match           86.8%;  Score 664;  DB 2;  Length 144;
  Best Local Similarity   98.4%;  Pred. No. 9.8e-54;
  Matches  125;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         18 APGRSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         78 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQTITFESFKENLKDFLLVIPFD 137

Qy        136 CWEPVQE 142
              |||||||
Db        138 CWEPVQE 144


RESULT 3
Q9GL44
ID   Q9GL44      PRELIMINARY;      PRT;   144 AA.
AC   Q9GL44;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor.
GN   Name=GM-CSF;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21479645; PubMed=11596094; DOI=10.1002/jmv.2073.abs;
RA   Hutchinson K.L., Villinger F., Miranda M.E., Ksiazek T.G.,
RA   Peters C.J., Rollin P.E.;
RT   "Multiplex analysis of cytokines in the blood of cynomolgus macaques
RT   naturally infected with Ebola virus (Reston serotype).";
RL   J. Med. Virol. 65:561-566(2001).
DR   EMBL; AY007376; AAG16626.1; -.
DR   HSSP; P04141; 2GMF.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
SQ   SEQUENCE   144 AA;  16177 MW;  7D5F381DA2FC832F CRC64;

  Query Match           85.4%;  Score 653;  DB 2;  Length 144;
  Best Local Similarity   95.3%;  Pred. No. 1e-52;
  Matches  121;  Conservative    5;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||||||| |||||||||||||||||||||||||:||||:|||||||||:|||||||
Db         18 APARSPSPGTQPWEHVNAIQEARRLLNLSRDTAAEMNKTVEVVSEMFDLQEPSCLQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||:|||||||||||||||||||||||||||||||||:||||:||||||||||||
Db         78 LYKQGLQGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFQSFKENLKDFLLVIPFD 137

Qy        136 CWEPVQE 142
              |||||||
Db        138 CWEPVQE 144


RESULT 4
Q865Y5
ID   Q865Y5      PRELIMINARY;      PRT;   144 AA.
AC   Q865Y5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor precursor.
GN   Name=GM-CSF;
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Villinger F.;
RL   Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY234216; AAO85329.1; -.
DR   HSSP; P04141; 2GMF.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
KW   Signal.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18    144       granulocyte-macrophage colony-stimulating
FT                                factor precursor.
SQ   SEQUENCE   144 AA;  16220 MW;  2321CAE533040D04 CRC64;

  Query Match           82.7%;  Score 633;  DB 2;  Length 144;
  Best Local Similarity   92.1%;  Pred. No. 7.4e-51;
  Matches  117;  Conservative    7;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||| |||  |||||||||||||||||||||||:||||:|||||||||:|:|||||
Db         18 APARLPSPGMQPWEHVNAIQEARRLLNLSRDTAAEMNKTVEVVSEMFDLQEPSCVQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||:|||||||||||||||||||||||||||||||||:||||:||||||||||||
Db         78 LYKQGLQGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFQSFKEDLKDFLLVIPFD 137

Qy        136 CWEPVQE 142
              |||||||
Db        138 CWEPVQE 144


RESULT 5
CSF2_SHEEP
ID   CSF2_SHEEP     STANDARD;      PRT;   144 AA.
AC   P28773;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE   (Colony-stimulating factor) (CSF).
GN   Name=CSF2;
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92039044; PubMed=1937025; DOI=10.1016/0378-1119(91)90163-6;
RA   McInnes C.J., Haig M.C.K.;
RT   "Cloning and expression of a cDNA encoding ovine granulocyte-
RT   macrophage colony-stimulating factor.";
RL   Gene 105:275-279(1991).
CC   -!- FUNCTION: Cytokine that stimulates the growth and differentiation
CC       of hematopoietic precursor cells from various lineages, including
CC       granulocytes, macrophages, eosinophils and erythrocytes (By
CC       similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GM-CSF family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X53561; CAA37632.1; -.
DR   PIR; JH0469; JH0469.
DR   HSSP; P04141; 2GMF.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL       1     17       By similarity.
FT   CHAIN       18    144       Granulocyte-macrophage colony-stimulating
FT                               factor.
FT   DISULFID     71    113      By similarity.
FT   DISULFID    105    138      By similarity.
FT   CARBOHYD     44     44      N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   144 AA;  16318 MW;  ABAAC8733B580008 CRC64;

  Query Match             71.6%;  Score 548;  DB 1;  Length 144;
  Best Local Similarity   80.3%;  Pred. No. 5.7e-43;
  Matches  102;  Conservative   10;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | ||| |:||:||:||:||  ||| | |||| |:|||||:||||| ||||||||||
Db         18 APTRQPSPVTRPWQHVDAIKEALSLLNDSTDTAAVMDETVEVVSEMFDSQEPTCLQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||| | | |||||||||:||||| |||| ||||||:|||||||||| :||||
Db         78 LYKQGLRGSLTSLTGSLTMMASHYKKHCPPTQETSCETQIITFKSFKENLKDFLFIIPFD 137

Qy        136 CWEPVQE 142
              |||||||
Db        138 CWEPVQK 144


RESULT 6
Q9MYK4
ID   Q9MYK4      PRELIMINARY;      PRT;   144 AA.
AC   Q9MYK4;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor (Fragment).
OS   Ovis aries (Sheep).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Caprinae; Ovis.
OX   NCBI_TaxID=9940;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91331592; PubMed=1869289;
RA   O'Brien P.M., Rothel J.S., Seow H.F., Wood P.R.;
RT   "Cloning and sequencing of the cDNA for ovine granulocyte-Macrophage
RT   colony stimulating factor (GM-CSF).";
RL   Immunol. Cell Biol. 69:51-55(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   O'Brien P.;
RL   Submitted (OCT-1990) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; X55991; CAA39463.1; -.
DR   PIR; A61632; A61632.
DR   HSSP; P04141; 2GMF.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
FT   CHAIN        1   >144       granulocyte-macrophage colony-stimulating
FT                               factor.
FT   NON_TER    144    144
SQ   SEQUENCE   144 AA;  16290 MW;  ABAAD7633B580008 CRC64;

  Query Match             71.1%;  Score 544;  DB 2;  Length 144;
  Best Local Similarity   79.5%;  Pred. No. 1.3e-42;
  Matches  101;  Conservative   10;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | ||| |:||:||:||:||  ||| | |||| |:|||||:||||| ||||||||||
Db         18 APTRQPSPVTRPWQHVDAIKEALSLLNDSTDTAAVMDETVEVVSEMFDSQEPTCLQTRLE 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||| | | |||||||||:||||| |||| ||||||:|||||||||| :||||
Db         78 LYKQGLRGSLTSLTGSLTMMASHYKKHCPPTQETSCETQIITFKSFKENLKDFLFIIPFD 137

Qy        136 CWEPVQE 142
              |||| |:
Db        138 CWEPAQK 144


RESULT 7
CSF2_CEREL
ID   CSF2_CEREL     STANDARD;      PRT;   144 AA.
AC   P51748;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE   (Colony-stimulating factor) (CSF).
GN   Name=CSF2;
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC   Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lockhart E.A.;
RL   Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that stimulates the growth and differentiation
CC       of hematopoietic precursor cells from various lineages, including
CC       granulocytes, macrophages, eosinophils and erythrocytes (By
CC       similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
```

```
CC   -!- SIMILARITY: Belongs to the GM-CSF family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U14392; AAA21439.1; -.
DR   HSSP; P04141; 2GMF.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     17       By similarity.
FT   CHAIN        18    144       Granulocyte-macrophage colony-stimulating
FT                                factor.
FT   DISULFID     71    113       By similarity.
FT   DISULFID    105    138       By similarity.
FT   CARBOHYD     44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     54     54       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   144 AA;  16283 MW;  1F5FF5FD03C94394 CRC64;

  Query Match             69.0%;  Score 528;  DB 1;  Length 144;
  Best Local Similarity   77.2%;  Pred. No. 4.1e-41;
  Matches   98;  Conservative   10;  Mismatches   19;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || |  || |:||:||:||:||  ||| | |||| |||||||:||||| ||||||||||:
Db         18 APTRPASPVTRPWQHVDAIKEALSLLNHSSDTAAVMNETVEVVSEMFDSQEPTCLQTRLK 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||| | | ||||| ||:|||||| |||| || |||:|||||||||| :||||
Db         78 LYKQGLRGSLTSLSGSLTMMARHYEQHCPPTQETSCETQTITFKSFKENLKDFLFIIPFD 137

Qy        136 CWEPVQE 142
              |||| |:
Db        138 CWEPAQK 144


RESULT 8
Q8WN17
ID   Q8WN17      PRELIMINARY;      PRT;   146 AA.
AC   Q8WN17;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor (Fragment).
GN   Name=GM-CSF;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vecchione A., D'Mello F., Kanellos T.S., Howard C.R., Hamblin A.S.,
RA   Catchpole B.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF448481; AAL41017.2; -.
DR   HSSP; P04141; 2GMF.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
FT   NON_TER     146    146
SQ   SEQUENCE   146 AA;  16604 MW;  B92D0617F391281C CRC64;

  Query Match             68.9%;  Score 527;  DB 2;  Length 146;
  Best Local Similarity   77.2%;  Pred. No. 5.1e-41;
  Matches   98;  Conservative   13;  Mismatches   16;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | ||| |:||:||:||:||  ||| | |||| |||||||:|| || :| |||||||:
Db         18 APTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVVSETFDAEELTCLQTRLK 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||| ||:||||||||||||||| |||||||:|||:|||:||||||  ||||
Db         78 LYKQGLRGSLIKLEGPLTMMASHYKQHCPPTLETSCATQMITFKSFKKNLKDFLFEIPFD 137

Qy        136 CWEPVQE 142
              ||:| |:
Db        138 CWKPAQK 144


RESULT 9
Q95L10
ID   Q95L10      PRELIMINARY;      PRT;   152 AA.
AC   Q95L10;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating-factor.
GN   Name=GM-CSF;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Mauel S., Commandeur U., Steinbach F.;
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY040203; AAK72108.2; -.
DR   HSSP; P04141; 2GMF.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
SQ   SEQUENCE   152 AA;  17173 MW;  75605CC1ADE9EFE9 CRC64;

  Query Match             67.1%;  Score 513;  DB 2;  Length 152;
  Best Local Similarity   78.7%;  Pred. No. 1.1e-39;
  Matches   96;  Conservative   11;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | ||| |:||:||:||:||  ||| | |||| |||||||:|| || :| |||||||:
Db         18 APTRQPSPVTRPWQHVDAIKEALSLLNNSSDTAAIMNETVEVVSETFDAEELTCLQTRLK 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||| ||:||||||||||||||| |||||||:|||:|||:||||||  ||||
Db         78 LYKQGLRGSLIKLEGPLTMMASHYKQHCPPTLETSCATQMITFKSFKKNLKDFLFEIPFD 137

Qy        136 CW 137
              ||
Db        138 CW 139


RESULT 10
CSF2_PIG
ID   CSF2_PIG       STANDARD;      PRT;   144 AA.
AC   Q29118; Q29046;
```

```
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE   (Colony-stimulating factor) (CSF).
GN   Name=CSF2;
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RA   Foss D.L., Murtaugh M.P.;
RL   Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Gloster S.E., Sandeman R.M., Strom A.D.G.;
RL   Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96167041; PubMed=8595928;
RA   Inumaru S., Takamatsu H.;
RT   "cDNA cloning of porcine granulocyte-macrophage colony-stimulating
RT   factor.";
RL   Immunol. Cell Biol. 73:474-476(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Cho Y.W., Choi I.-S., Yoo H.S.;
RT   "Cloning of porcine granulocyte macrophage-colony stimulating factor
RT   in alveolar macrophages.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that stimulates the growth and differentiation
CC       of hematopoietic precursor cells from various lineages, including
CC       granulocytes, macrophages, eosinophils and erythrocytes (By
CC       similarity).
CC   -!- SUBUNIT: Monomer.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GM-CSF family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U61139; AAB03867.1; -.
DR   EMBL; U67318; AAB49939.1; -.
DR   EMBL; U67175; AAB06854.1; -.
DR   EMBL; D21074; BAA04649.1; -.
DR   EMBL; AY116504; AAM48280.1; -.
DR   HSSP; P04141; 2GMF.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     17       Potential.
FT   CHAIN        18    144       Granulocyte-macrophage colony-stimulating
FT                                factor.
FT   DISULFID     71    113       By similarity.
FT   DISULFID    105    138       By similarity.
FT   CARBOHYD     44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     47     47       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     54     54       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     59     59       V -> I (in Ref. 2).
FT   CONFLICT    140    140       G -> E (in Ref. 2).
FT   CONFLICT    142    143       VK -> AQ (in Ref. 2).
SQ   SEQUENCE   144 AA;  16254 MW;  793DACB62CF736D0 CRC64;

  Query Match             63.7%;  Score 487;  DB 1;  Length 144;
  Best Local Similarity   70.1%;  Pred. No. 2.6e-37;
  Matches   89;  Conservative   16;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | ||| |:||:||:||:||  ||| | |||| |||||:|: |||| |||||:||||
Db         18 APTRPPSPVTRPWQHVDAIKEALSLLNNSNDTAAVMNETVDVVCEMFDPQEPTCVQTRLN 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||||:|| |||::| ||:|||| | |||| || |||:|||::|  ||  ||||
Db         78 LYKQGLRGSLTRLKSPLTLLAKHYEQHCPLTEETSCETQSITFKSFKDSLNKFLFTIPFD 137

Qy        136 CWEPVQE 142
              || ||::
Db        138 CWGPVKK 144


RESULT 11
Q6Q8A7
ID   Q6Q8A7      PRELIMINARY;      PRT;   143 AA.
AC   Q6Q8A7;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Granulocyte macrophage colony stimulating factor.
OS   Bubalus bubalis (Domestic water buffalo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bubalus.
OX   NCBI_TaxID=89462;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dhinakar Raj G., HariShankar M., Thennarasu S., Mahalinga Nainar A.;
RL   Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY553190; AAS59070.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
SQ   SEQUENCE   143 AA;  16105 MW;  274532FF0FFE4C3F CRC64;

  Query Match             63.6%;  Score 486.5;  DB 2;  Length 143;
  Best Local Similarity   70.1%;  Pred. No. 2.9e-37;
  Matches   89;  Conservative   18;  Mismatches   19;  Indels    1;  Gaps    1;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | ||  |:||:||:||:||  ||| | :  | ||:| ||:||||| ||||||||||:
Db         18 APTRPPSTVTRPWQHVDAIKEALSLLNQSSEPDAGMNDT-EVVSEMFDAQEPTCLQTRLK 76

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||:||:|||| | | |||||:||::|||||||||| || |||:||||:||:|| :||||
Db         77 LYKKGLQGSLTSLMGSLTMMATHYEKHCPPTPETSCGTQFITFKSFKEDLKEFLFIIPFD 136

Qy        136 CWEPVQE 142
              |||| |:
Db        137 CWEPAQK 143


RESULT 12
CSF2_BOVIN
ID   CSF2_BOVIN     STANDARD;      PRT;   143 AA.
AC   P11052;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-JUL-1989 (Rel. 11, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
```

```
DE   Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE   (Colony-stimulating factor) (CSF).
GN   Name=CSF2;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=89096971; PubMed=3062386; DOI=10.1016/0161-5890(88)90120-4;
RA   Maliszewski C.R., Schoenborn M.A., Cerretti D.P., Wignall J.M.,
RA   Picha K.S., Cosman D., Tushinski R.J., Gillis S., Baker P.E.;
RT   "Bovine GM-CSF: molecular cloning and biological activity of the
RT   recombinant protein.";
RL   Mol. Immunol. 25:843-850(1988).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90021093; PubMed=2678728; DOI=10.1016/0165-2427(89)90036-6;
RA   Leong S.R., Flaggs G.M., Lawman M.J.P., Gray P.W.;
RT   "Cloning and expression of the cDNA for bovine granulocyte-macrophage
RT   colony-stimulating factor.";
RL   Vet. Immunol. Immunopathol. 21:261-278(1989).
CC   -!- FUNCTION: Cytokine that stimulates the growth and differentiation
CC       of hematopoietic precursor cells from various lineages, including
CC       granulocytes, macrophages, eosinophils and erythrocytes (By
CC       similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GM-CSF family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U22385; AAA66075.1; -.
DR   PIR; JL0037; FQBOGM.
DR   HSSP; P04141; 2GMF.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL       1     17
FT   CHAIN       18    143       Granulocyte-macrophage colony-stimulating
FT                               factor.
FT   DISULFID    70    112       By similarity.
FT   DISULFID   104    137       By similarity.
FT   CARBOHYD    44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    54     54       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   143 AA;  16157 MW;  4A24E26A870A51EC CRC64;

  Query Match          62.8%;  Score 480.5;  DB 1;  Length 143;
  Best Local Similarity   68.5%;  Pred. No. 1e-36;
  Matches   87;  Conservative   20;  Mismatches   19;  Indels    1;  Gaps    1;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || | |: :|:||:||:||:||  ||| | || | ||:| ||:|| || ||||||||||:
Db         18 APTRPPNTATRPWQHVDAIKEALSLLLNHSSDTDAVMNDT-EVVSEKFDSQEPTCLQTRLK 76

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||| ||:|||| | | |||||:||::|||||||||| || |:|::|||:||:|| :||||
Db         77 LYKNGLQGSLTSLMGSLTMMATHYEKHCPPTPETSCGTQFISFKNFKEDLKEFLFIIPFD 136

Qy        136 CWEPVQE 142
              |||| |:
Db        137 CWEPAQK 143


RESULT 13
CSF2_CANFA
ID   CSF2_CANFA     STANDARD;      PRT;   144 AA.
AC   P48749;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE   (Colony-stimulating factor) (CSF).
GN   Name=CSF2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91329842; PubMed=1868252;
RA   Nash R.A., Schuening F., Appelbaum F.R., Hammond W.P., Boone T.,
RA   Morris C.F., Slichter S.J., Storb R.;
RT   "Molecular cloning and in vivo evaluation of canine granulocyte-
RT   macrophage colony-stimulating factor.";
RL   Blood 78:930-937(1991).
CC   -!- FUNCTION: Cytokine that stimulates the growth and differentiation
CC       of hematopoietic precursor cells from various lineages, including
CC       granulocytes, macrophages, eosinophils and erythrocytes (By
CC       similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GM-CSF family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S49738; AAB19466.1; -.
DR   PIR; A44936; A44936.
DR   HSSP; P04141; 2GMF.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL       1     17       By similarity.
FT   CHAIN       18    144       Granulocyte-macrophage colony-stimulating
FT                               factor.
FT   DISULFID    71    113       By similarity.
FT   DISULFID   105    138       By similarity.
FT   CARBOHYD    44     44       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   144 AA;  16137 MW;  6323807E1F1C6343 CRC64;

  Query Match          61.8%;  Score 473;  DB 1;  Length 144;
  Best Local Similarity   68.5%;  Pred. No. 5.2e-36;
  Matches   87;  Conservative   19;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              || |||:  |:| :||:|||||  ||| | |  | ||: |:|:||:|| : ||||:|||:
Db         18 APTRSPTLVTRPSQHVDAIQEALSLLNNSNDVTAVMNKAVKVVSEVFDPEGPTCLETRLQ 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||:||:|||| || ||||||:||||||||||: |||| | |:||||||||||  ||||
Db         78 LYKEGLQGSLTSLKNPLTMMANHYKQHCPPTPESPCATQNINFKSFKENLKDFLFNIPFD 137

Qy        136 CWEPVQE 142
Db        137 CWEPAQK 143
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              ||:||::
Db        138 CWKPVKK 144


RESULT 14
Q7YRF7
ID   Q7YRF7      PRELIMINARY;      PRT;   141 AA.
AC   Q7YRF7;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor (Fragment).
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Dunham S.P., Bruce J., Jarrett O.;
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY138140; AAN11308.1; -.
DR   HSSP; P04141; 1CSG.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005129; F:granulocyte macrophage colony-stimulating f. . .; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   141 AA;  16039 MW;  D7E78E3DA77C1F66 CRC64;

  Query Match             61.7%;  Score 472;  DB 2;  Length 141;
  Best Local Similarity   69.3%;  Pred. No. 6.2e-36;
  Matches   88;  Conservative   14;  Mismatches   25;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              ||  |||  |:||:||:||:||  ||| | :  | ||| |||:||||| :|| |||| |:
Db         15 APTSSPSSVTRPWQHVDAIKEALSLLNNSSEITAVMNEAVEVVSEMFDPEEPKCLQTHLK 74

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||:|||||||  || || |||:||||||| |||| | || |||::|||||||||  ||||
Db         75 LYEQGLRGSLISLKEPLRMMANHYKQHCPLTPETPCETQTITFKNFKENLKDFLFNIPFD 134

Qy        136 CWEPVQE 142
              ||:|||:
Db        135 CWKPVQK 141


RESULT 15
CSF2_FELCA
ID   CSF2_FELCA     STANDARD;      PRT;   144 AA.
AC   O62757;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Granulocyte-macrophage colony-stimulating factor precursor (GM-CSF)
DE   (Colony-stimulating factor) (CSF).
GN   Name=CSF2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Hughes K.J., O'Reilly K.L.;
RL   Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that stimulates the growth and differentiation
CC       of hematopoietic precursor cells from various lineages, including
CC       granulocytes, macrophages, eosinophils and erythrocytes (By
CC       similarity).
CC   -!- SUBUNIT: Monomer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the GM-CSF family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF053007; AAC06041.1; -.
DR   HSSP; P04141; 2GMF.
DR   InterPro; IPR009079; 4_helix_cytokine.
DR   InterPro; IPR000773; GM_CSF.
DR   Pfam; PF01109; GM_CSF; 1.
DR   PRINTS; PR00693; GMCSFACTOR.
DR   ProDom; PD007349; GM_CSF; 1.
DR   SMART; SM00040; CSF2; 1.
DR   PROSITE; PS00702; GM_CSF; 1.
KW   Cytokine; Glycoprotein; Growth factor; Signal.
FT   SIGNAL        1     17       By similarity.
FT   CHAIN        18    144       Granulocyte-macrophage colony-stimulating
FT                                factor.
FT   DISULFID     71    113       By similarity.
FT   DISULFID    105    138       By similarity.
FT   CARBOHYD     44     44       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     45     45       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     54     54       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   144 AA;  16505 MW;  42C5BF5F8235DA55 CRC64;

  Query Match             59.0%;  Score 451;  DB 1;  Length 144;
  Best Local Similarity   66.9%;  Pred. No. 5.7e-34;
  Matches   85;  Conservative   14;  Mismatches   28;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              ||  |||  |:||:||:|::||  ||| | :  | |||||||:||||| :|| |||| |:
Db         18 APTSSPSSVTRPWQHVDAMKEALSLLNNSSEITAVMNETVEVVSEMFDPEEPKCLQTHLK 77

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||:|||||||  || || |||:||||||| |||| | || |||::||| |||||   |||
Db         78 LYEQGLRGSLISLKEPLRMMANHYKQHCPLTPETPCETQTITFKNFKEKLKDFLFNNPFD 137

Qy        136 CWEPVQE 142
              || | |:
Db        138 CWGPDQK 144


Search completed: March  8, 2005, 16:13:25
Job time : 179 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 8, 2005, 15:55:38 ; Search time 164 Seconds
(without alignments)
334.878 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHHHSSGIEGRMAPARS.....ENLKDFLLVIPFDCWEPVQE 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	682	89.2	259	2	AAR79317	Aar79317 IL-3 cont
2	682	89.2	259	3	AAY53198	Aay53198 Human int
3	682	89.2	259	4	AAE13992	Aae13992 Myelopoie
4	682	89.2	259	5	ABG97765	Abg97765 Human Int
5	682	89.2	259	8	ADJ14353	Adj14353 Chimera p
6	679	88.8	533	2	AAW19763	Aaw19763 p53-GM-CS
7	678	88.6	128	1	AAP90118	Aap90118 Synthetic
8	678	88.6	128	1	AAP90115	Aap90115 Synthetic
9	678	88.6	128	2	AAR79338	Aar79338 pMON13012
10	678	88.6	128	2	AAW00103	Aaw00103 Granulocy
11	678	88.6	128	3	AAY53217	Aay53217 Human G-C
12	678	88.6	128	4	AAE14011	Aae14011 Chemicall
13	678	88.6	128	5	ABG97784	Abg97784 Human Int
14	678	88.6	128	8	ADJ14372	Adj14372 Protein r
15	678	88.6	274	2	AAR79320	Aar79320 IL-3 cont
16	678	88.6	274	3	AAY53201	Aay53201 Human int
17	678	88.6	274	4	AAE13995	Aae13995 Myelopoie
18	678	88.6	274	5	ABG97768	Abg97768 Human Int
19	678	88.6	274	8	ADJ14356	Adj14356 Chimera p
20	678	88.6	301	2	AAR79318	Aar79318 IL-3 cont
21	678	88.6	301	3	AAY53199	Aay53199 Human int
22	678	88.6	301	4	AAE13993	Aae13993 Chemicall
23	678	88.6	301	5	ABG97766	Abg97766 Human Int
24	676	88.4	523	3	AAY44994	Aay44994 HD70scFv-
25	675	88.2	712	8	ADL16720	Adl16720 Human stu
26	675	88.2	736	7	ADF15029	Adf15029 Human alb
27	675	88.2	736	7	ADF14935	Adf14935 Human alb
28	674.5	88.2	736	7	ADF14936	Adf14936 Human alb
29	674	88.1	128	2	AAR03199	Aar03199 New human
30	673	88.0	127	2	AAR13215	Aar13215 Oxidised
31	673	88.0	127	2	AAR41540	Aar41540 r-h-GM-CS
32	673	88.0	127	3	AAY69025	Aay69025 Amino aci
33	673	88.0	127	4	AAE13117	Aae13117 Mature hu
34	673	88.0	127	5	ABB78399	Abb78399 Amino aci
35	673	88.0	127	7	ADF70845	Adf70845 Human mac
36	673	88.0	127	8	ADL88868	Adl88868 Human cyt
37	673	88.0	128	2	AAW00102	Aaw00102 Granulocy
38	673	88.0	131	1	AAP70351	Aap70351 Sequence
39	673	88.0	131	5	ABB08135	Abb08135 Human GMC
40	673	88.0	131	5	ABG31632	Abg31632 Human gra
41	673	88.0	131	5	AAO19090	Aao19090 Human gra
42	673	88.0	143	8	ADJ36195	Adj36195 Self-coal
43	673	88.0	144	1	AAP60418	Aap60418 Human gra
44	673	88.0	144	1	AAP70657	Aap70657 Sequence
45	673	88.0	144	2	AAR04098	Aar04098 Metapyroc

ALIGNMENTS

RESULT 1
AAR79317
ID AAR79317 standard; protein; 259 AA.
XX
AC AAR79317;
XX
DT 25-AUG-1999 (first entry)
XX
DE IL-3 containing fusion protein.
XX
KW interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW mutant; mutein; fusion protein.
XX
OS Synthetic.
XX
PN WO9521254-A1.
XX
PD 10-AUG-1995.
XX
PF 02-FEB-1995; 95WO-US001185.
XX
PR 04-FEB-1994; 94US-00192325.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 1995-283774/37.
DR N-PSDB; AAQ97169.
XX
PT Fusion proteins comprising a human interleukin-3 variant, a linker and
PT interleukin-3, a variant or a colony stimulating factor - useful to
PT increase haematopoietic cell prodn. in a mammal.
XX
PS Claim 16; Page 86; 447pp; English.
XX
CC A new fusion protein has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L
CC -R1 or R1-R1, in which R1 is a mutant or variant of human interleukin-3
CC (hIL-3) having the present generic sequence, R2 is a second colony
CC stimulating factor (CSF) including cytokine, lymphokine, interleukin,
CC haematopoietic growth factor or IL-3 variant, and L is a linker. The
CC present sequence corresponds to native hIL-3(1-133) in which 1-14 amino
CC acids may be deleted from the N-terminal, 1-15 amino acids can be deleted
CC from the C-terminal, and at least 4 and up to 44 amino acids in the
CC region 17-123 are different from those in the native protein. The fusion
CC protein is used to increase haematopoietic cell production. It is also
CC useful as an IL-3 antagonist or as a discrete antigenic fragment for

CC production of antibodies useful in immunoassays and immunotherapy.
CC Antagonists are used to block the growth of certain cancer cells and in
CC treatment of asthma. The fusion protein can also be used to stimulate
CC bone marrow and blood cell activation and growth in vitro before infusion
CC ; and to treat diseases characterised by decreased levels of myeloid,
CC erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic
CC system. The protein has the usual activity of both its component
CC proteins, but may have increased synergistic activity and reduced
CC undesired side effects
XX
SQ Sequence 259 AA;

Query Match 89.2%; Score 682; DB 2; Length 259;
Best Local Similarity 97.0%; Pred. No. 2.2e-64;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
              ||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy         69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy        129 LLVIPFDCWEPVQE 142
              ||||||||||||||
Db        246 LLVIPFDCWEPVQE 259
```

RESULT 2
AAY53198
ID AAY53198 standard; protein; 259 AA.
XX
AC AAY53198;
XX
DT 19-MAY-2000 (first entry)
XX
DE Human interleukin-3 mutant containing fusion protein SEQ ID NO:141.
XX
KW Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
KW colony stimulating factor; haematopoietic growth factor; lymphokine;
KW fusion protein; haematopoietic disorder; infection; cancer;
KW radiation therapy; chemotherapy; bone marrow suppressive drug;
KW bone marrow activation; blood cell activation; blood transplant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6022535-A.
XX
PD 08-FEB-2000.
XX
PF 06-JUN-1995; 95US-00469318.
XX
PR 04-FEB-1994; 94US-00192325.
PR 02-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Easton AM, Klein BK;
PI Paik K, Thomas JW, Mckearn JP, Olins PO, Caparon MH;
XX
DR WPI; 2000-160368/14.
XX
PT Treating hematopoietic disorders with fusion proteins comprising mutated
PT interleukin-3 fused with secondary colony stimulating factors or other
PT interleukin-3 variants.
XX
PS Example 27; Col 71-72; 276pp; English.
XX
CC Methods have been developed for treating haematopoietic disorders with
CC fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-
CC 3) variants or mutant proteins (muteins) fused with secondary colony
CC stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
CC and/or haematopoietic colony stimulating factors) or other interleukin-3
CC variants with or without a linker. The methods may be used in vivo to
CC treat haematopoietic disorders resulting from bacterial, viral and fungal
CC infections, cancer radiation therapy, chemotherapy or bone marrow
CC suppressive drugs. They may also be used in vitro to stimulate bone
CC marrow and blood cell activation and growth prior to infusion of the bone
CC marrow and blood transplants into patients. IL-3 is a haematopoietic
CC growth factor which has the property of being able to promote the
CC survival, growth and differentiation of haematopoietic cells. The fusion
CC molecules are characterised by possessing the usual activity of both of
CC their constituent peptides and further by having a biological or
CC physiological activity greater than the additive function of the IL-3 or
CC second CSF alone (i.e. the peptides act synergistically). Their activity
CC may also be further enhanced by the mutations they comprise. The
CC variations may further reduce undesirable side effects associated with IL
CC -3. AAY53130 to AAY53226, and AAA03721 to AAA03782 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 259 AA;

Query Match 89.2%; Score 682; DB 3; Length 259;
Best Local Similarity 97.0%; Pred. No. 2.2e-64;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
              ||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy         69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy        129 LLVIPFDCWEPVQE 142
              ||||||||||||||
Db        246 LLVIPFDCWEPVQE 259
```

RESULT 3
AAE13992
ID AAE13992 standard; protein; 259 AA.
XX
AC AAE13992;
XX
DT 26-FEB-2002 (first entry)
XX
DE Myelopoietin (MPO) protein #127.
XX
KW Myelopoietin conjugate; MPO; immunosuppressive; vulnerary; antiparasitic;
KW antibacterial; virucide; interleukin-3; IL-3; haematopoietic disorder;
KW haematopoietic growth factor receptor; neutropenia; thrombocytopenia;
KW leukopenia; anaemia; chemotherapy; bone marrow transplantation; burn;
KW radiation therapy; haematopoietic progenitor mobilisation; infection;
KW wound healing.
XX
OS Unidentified.
XX
PN WO200176639-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US011256.
XX
PR 06-APR-2000; 2000US-0195496P.
XX
PA (PHAA) PHARMACIA CORP.
PA (FINN/) FINN R.
PA (GOKA/) GOKARN Y.
PA (HILL/) HILLS R.
PA (NICA/) NICASTRO P.
PA (QIHH/) QI H.
PA (SEDO/) SEDO K.

PA (SIEG/) SIEGEL N.
PA (WALT/) WALTER S.
XX
PI Finn R, Gokarn Y, Hills R, Nicastro P, Qi H, Sedo K, Siegel N;
PI Walter S;
XX
DR WPI; 2001-657130/75.
XX
PT Myelopoietin conjugate for treating e.g. leukopenia comprises a water-
PT soluble polymer attached to the protein.
XX
PS Claim 5; Page 197-198; 429pp; English.
XX
CC The invention relates to chemically modified myelopoietin (MPO)
CC conjugates having at least one water-soluble polymer molecule covalently
CC attached, via activating group, to at least one amino acid residue of a
CC biologically active myelopoietin polypeptide. MPOs are multifunctional
CC agonists of human interleukin-3 (IL-3) and another haematopoietic growth
CC factor receptor. Sequences of the invention are useful for treating
CC haematopoietic disorders (e.g. neutropenia, leukopenia, thrombocytopenia
CC and anaemia), including those arising from chemotherapy and radiation
CC therapy. MPOs are also useful in bone marrow transplantation, wound
CC healing, burn treatment and the treatment of parasite, bacterial or viral
CC infection. They are useful for mobilising haematopoietic progenitors and
CC stem cells. The chemically modified MPOs have a longer lasting neutrophil
CC -releasing activity, decreased clearance rate, increased stability and
CC decreased antigenicity than unmodified myelopoietins. The present
CC sequence is a myelopoietin protein
XX
SQ Sequence 259 AA;

Query Match 89.2%; Score 682; DB 4; Length 259;
Best Local Similarity 97.0%; Pred. No. 2.2e-64;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy 69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy 129 LLVIPFDCWEPVQE 142
||||||||||||||
Db 246 LLVIPFDCWEPVQE 259

RESULT 4
ABG97765
ID ABG97765 standard; protein; 259 AA.
XX
AC ABG97765;
XX
DT 18-DEC-2002 (first entry)
XX
DE Human Interleukin-3 chimaeric protein #20.
XX
KW Human; interleukin-3; IL-3; mutant; mutein; stem cell;
KW haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; G-CSF;
KW G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
KW human growth hormone; B-cell growth factor; leukaemia;
KW B-cell differentiation factor; eosinophil differentiation factor;
KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
KW myelofibrosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6436387-B1.
XX
PD 20-AUG-2002.
XX
PF 09-DEC-1996; 96US-00762227.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 04-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2002-749206/81.
XX
PT Ex vivo expansion of stem cells, for enhancing transduction efficiency of
PT cultured stem cells, comprises culturing stem cells in growth medium
PT having mutant interleukin-3, and hematopoietic factor, and harvesting
PT cultured cells.
XX
PS Claim 8; Col 247-250; 203pp; English.
XX
CC The invention relates to ex vivo expansion of stem cells, comprises
CC culturing stem cells with a growth medium comprising a chimaera protein,
CC and harvesting the cultured stem cells. The chimaera is based on a
CC mutated human interleukin-3 (IL_3) sequence coupled to a haematopoietic
CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
CC CSFSer17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
CC differentiation factor, eosinophil differentiation factor and stem cell
CC factor (SCF)) via a peptide linker. The formula for the chimaera is given
CC in the specification. Also included is a method for enhancing the
CC efficiency of the transduction of cultured stem cells by a heterologous
CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
CC culturing the stem cells with a growth medium comprising the chimaera (c)
CC transducing DNA into cultured cells; and (d) harvesting the transduced
CC cells. The method is useful for ex vivo expansion of stem cells, and
CC enhancing the efficiency of the transduction of cultured stem cells by a
CC heterologous gene. The method is also useful for treating a patient
CC having a haematopoietic disorder. The expanded haematopoietic cells are
CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
CC and myelofibrosis. The present sequence is a human IL-3
CC mutant/haematopoietic factor chimaeric sequence
XX
SQ Sequence 259 AA;

Query Match 89.2%; Score 682; DB 5; Length 259;
Best Local Similarity 97.0%; Pred. No. 2.2e-64;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
|| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy 69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy 129 LLVIPFDCWEPVQE 142
||||||||||||||
Db 246 LLVIPFDCWEPVQE 259

RESULT 5
ADJ14353
ID ADJ14353 standard; protein; 259 AA.
XX
AC ADJ14353;

XX
DT 20-MAY-2004 (first entry)
XX
DE Chimera protein related to human interleukin-3 mutant protein SEQ ID 141.
XX
KW stem cell; antianaemic; immunostimulant; immunomodulator;
KW antiinflammatory; dermatological; immunosuppressive; cytostatic;
KW neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;
KW lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
KW Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
KW myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; chimera.
XX
OS Unidentified.
XX
PN US2003185790-A1.
XX
PD 02-OCT-2003.
XX
PF 26-FEB-2002; 2002US-00083446.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 02-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
PR 09-DEC-1996; 96US-00762227.
XX
PA (BAUE/) BAUER S C.
PA (ABRA/) ABRAMS M A.
PA (BRAF/) BRAFORD-GOLDBERG S R.
PA (CAPA/) CAPARON M H.
PA (EAST/) EASTON A M.
PA (KLEI/) KLEIN B K.
PA (MCKE/) MCKEARN J P.
PA (OLIN/) OLINS P O.
PA (PAIK/) PAIK K.
PA (THOM/) THOMAS J W.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2004-096775/10.
XX
PT Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating
PT aplastic anemia, involves culturing the stem cells with growth medium
PT comprising chimera protein, and harvesting the cultured stem cells.
XX
PS Claim 8; SEQ ID NO 141; 202pp; English.
XX
CC The invention relates to a novel method whereby stem cells are ex vivo
CC expanded via culturing the stem cells with a growth medium comprising a
CC chimera protein, followed by harvesting of the cultured stem cells. The
CC method of the invention has antianaemic, immunostimulant,
CC immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC cytostatic and neuroprotective applications and may be useful to target
CC haemopoietic cells for gene therapy, preferably for treating patients
CC having a haemopoietic disorder characterised by decreased levels of
CC myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC system. The expanded ex vivo cells may be used to treat neutropenia,
CC aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC myelofibrosis. The current sequence is that of a chimera protein related
CC to the human interleukin-3 (IL-3) mutant protein of the invention.
XX
SQ Sequence 259 AA;

Query Match 89.2%; Score 682; DB 8; Length 259;
Best Local Similarity 97.0%; Pred. No. 2.2e-64;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
|| ||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy 69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy 129 LLVIPFDCWEPVQE 142
||||||||||||||

Db 246 LLVIPFDCWEPVQE 259

RESULT 6
AAW19763
ID AAW19763 standard; protein; 533 AA.
XX
AC AAW19763;
XX
DT 17-SEP-1997 (first entry)
XX
DE p53-GM-CSF immunostimulant fusion protein.
XX
KW p53-GM-CSF; granulocyte macrophage colony stimulating factor;
KW tumour suppressor gene; immunostimulant; cancer; therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Protein 1. .393
FT /label= p53
FT Peptide 394. .395
FT /label= Linker
FT /note= "product of XbaI linker"
FT Protein 396. .524
FT /label= GM-CSF
FT Peptide 525. .533
FT /note= "hexahistidine tag"
XX
PN WO9724438-A1.
XX
PD 10-JUL-1997.
XX
PF 23-DEC-1996; 96WO-US020241.
XX
PR 28-DEC-1995; 95US-00579823.
XX
PA (ACTI-) ACTIVATED CELL THERAPY INC.
XX
PI Laus R, Ruegg CL, Wu H;
XX
DR WPI; 1997-363674/33.
DR N-PSDB; AAT72724.
XX
PT Potent APC that activates T-cells to give multivalent cellular immune
PT response - can also induce a cytotoxic T-cell response in a vertebrate
PT subject.
XX
PS Example 7; Fig 11; 45pp; English.
XX
CC A fusion protein (AAW19763) comprises human p53 tumour suppressor protein
CC and granulocyte-macrophage colony stimulating factor (GM- CSF). It is the
CC expression product of a nucleic acid molecule (AAT72724) prepd. by PCR
CC amplification of p53 cDNA GM-CSF cDNA sequences (the GM-CSF antisense
CC primer including a hexahistidine tag sequence) and their fusion via a
CC XbaI linker. Fusion expression vectors can be used to transfect mammalian
CC and insect cells. The p53-GM-CSF fusion protein is used to generate anti-
CC p53 immunity. Tumour cells are eliminated by cytotoxic T lymphocytes
CC activated in vivo or in vitro by exposure to antigen- presenting cells
CC exposed to the fusion protein
XX
SQ Sequence 533 AA;

Query Match 88.8%; Score 679; DB 2; Length 533;
Best Local Similarity 97.7%; Pred. No. 1.3e-63;

```
  Matches  128;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          12 EGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQ 71
               : | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         393 DSRSAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQ 452

Qy          72 TRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLV 131
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         453 TRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLV 512

Qy         132 IPFDCWEPVQE 142
               ||||||||||| 
Db         513 IPFDCWEPVQE 523


RESULT 7
AAP90118
ID   AAP90118 standard; protein; 128 AA.
XX
AC   AAP90118;
XX
DT   25-MAR-2003  (revised)
DT   01-NOV-1989  (first entry)
XX
DE   Synthetic human granulyte colony stimulating factor.
XX
KW   BspMI; restriction sites; blunt ends; fusion proteins; synthetic;
KW   human granulocyte colony stimulating factor.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   GB2212160-A.
XX
PD   19-JUL-1989.
XX
PF   13-NOV-1987;   87GB-00726581.
XX
PR   13-NOV-1987;   87GB-00026581.
XX
PA   (BRBI-) BRITISH BIO-TECHN L.
XX
PI   Edwards RM;
XX
DR   WPI; 1989-208959/29.
DR   N-PSDB; AAN90383.
XX
PT   DNA including recognition site for BspMI enzyme - allowing generation of
PT   blunt end for fusion in prodn. of fusion proteins.
XX
PS   Disclosure; Fig 2; 23pp; English.
XX
CC   Synthetic human granulocyte colony stimulating factor (GM-CSF) contg.
CC   useful restriction sites, and a BspMI site. See corresp. AAN90383. Its
CC   DNA is useful for generating blunt ends in fusion protein prodn. (Updated
CC   on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct
CC   PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 128 AA;

  Query Match           88.6%;  Score 678;  DB 1;  Length 128;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-64;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy          75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy         135 DCWEPVQE 142
               ||||||||
Db         121 DCWEPVQE 128


RESULT 8
AAP90115
ID   AAP90115 standard; protein; 128 AA.
XX
AC   AAP90115;
XX
DT   25-MAR-2003  (revised)
DT   01-NOV-1989  (first entry)
XX
DE   Synthetic human granulocyte colony stimulating factor.
XX
KW   Human granulocyte colony stimulating factor; Synthetic restriction sites;
KW   cassette mutagenesis; GM-CSF; expression system.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   GB2212159-A.
XX
PD   19-JUL-1989.
XX
PF   13-NOV-1987;   87GB-00026580.
XX
PR   13-NOV-1987;   87GB-00026580.
XX
PA   (BRBI-) BRITISH BIO-TECHN L.
XX
PI   Edwards RM;
XX
DR   WPI; 1989-208958/29.
XX
PT   Human granulocyte-macrophage colony stimulating factor - synthetic DNA
PT   includes restriction sites for cassette mutagenesis and incorporation in
PT   expression systems.
XX
PS   Claim 2; Fig 3a; 21pp; English.
XX
CC   Synthetic human granulocyte colony stimulating factor (GM-CSF), see
CC   corresp. AAN90274. Its DNA has useful restriction sites for: HindIII;
CC   BspMI; NcoI; BstEII; BsmI; EcoRV; BglI; ApaI; BalI; XmnI; BamHI; and
CC   EcoRI. Used to facilitate cassette mutagenesis of selected regions.
CC   Synthesised by phosphoramidite chemistry, by dividing desired gene into
CC   18 oligomers. (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 128 AA;

  Query Match           88.6%;  Score 678;  DB 1;  Length 128;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-64;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy          75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy         135 DCWEPVQE 142
               ||||||||
Db         121 DCWEPVQE 128


RESULT 9
AAR79338
ID   AAR79338 standard; protein; 128 AA.
XX
AC   AAR79338;
XX
```

```
DT   25-AUG-1999  (first entry)
XX
DE   pMON13012 peptide.
XX
KW   Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW   mutant; mutein; fusion protein.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9521254-A1.
XX
PD   10-AUG-1995.
XX
PF   02-FEB-1995;   95WO-US001185.
XX
PR   04-FEB-1994;   94US-00192325.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer CS,  Abrams MA,  Braford-Goldberg SR,  Caparon MH,  Easton AM;
PI   Klein BK,  Mckearn JP,  Olins PO,  Paik K,  Thomas JW;
XX
DR   WPI; 1995-283774/37.
DR   N-PSDB; AAQ97208.
XX
PT   Fusion proteins comprising a human interleukin-3 variant, a linker and
PT   interleukin-3, a variant or a colony stimulating factor - useful to
PT   increase haematopoietic cell prodn. in a mammal.
XX
PS   Example 20; Page 125; 447pp; English.
XX
CC   A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC   R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC   interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC   including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC   or IL-3 variant, and L is a linker. Generic sequences are described in
CC   AAW03235 - AAW03242, and specifically claimed examples are shown in
CC   AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC   recombinant DNA techniques. Specifically claimed examples of DNA
CC   sequences which encode these proteins are shown in AAQ97167-Q97204 and
CC   AAQ97222-Q97227. The fusion protein is used to increase haematopoietic
CC   cell production. It is also useful as an IL-3 antagonist or as a discrete
CC   antigenic fragment for production of antibodies useful in immunoassays
CC   and immunotherapy. Antagonists are used to block the growth of certain
CC   cancer cells and in treatment of asthma. The fusion protein can also be
CC   used to stimulate bone marrow and blood cell activation and growth in
CC   vitro before infusion; and to treat diseases characterised by decreased
CC   levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the
CC   haematopoietic system. The protein has the usual activity of both its
CC   component proteins, but may have increased synergistic activity and
CC   reduced undesired side effects
XX
SQ   Sequence 128 AA;

  Query Match             88.6%;  Score 678;  DB 2;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-64;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy        135 DCWEPVQE 142
              ||||||||
Db        121 DCWEPVQE 128


RESULT 10
AAW00103
ID   AAW00103 standard; protein; 128 AA.
XX
AC   AAW00103;
XX
DT   25-MAR-2003  (revised)
DT   11-FEB-1997  (first entry)
XX
DE   Granulocyte macrophage colony-stimulating factor (Ile101).
XX
KW   GM-CSF; granulocyte macrophage colony-stimulating factor; expression;
KW   construct; stable; production.
XX
OS   Homo sapiens.
XX
PN   JP08173185-A.
XX
PD   09-JUL-1996.
XX
PF   28-APR-1987;   95JP-00263370.
XX
PR   28-APR-1987;   87JP-00106148.
XX
PA   (AMGE-) AMGEN INC.
PA   (KIRI ) KIRIN BREWERY KK.
XX
DR   WPI; 1996-365600/37.
DR   N-PSDB; AAT34400.
XX
PT   Prodn. of human granulocyte macrophage colony-stimulating factor - by
PT   culturing E. coli transformed with human GM-CSF DNA.
XX
PS   Claim 1; Page 2; 16pp; Japanese.
XX
CC   The present sequence is that of human granulocyte macrophage colony-
CC   stimulating factor (hGM-CSF; n = 101, Ile). A series of oligonucleotides
CC   were synthesised and ligated together to form a stable expression
CC   construct. The technique is used for the efficient prodn. of a
CC   glycoprotein with hGM-CSF activity. (Updated on 25-MAR-2003 to correct PF
CC   field.)
XX
SQ   Sequence 128 AA;

  Query Match             88.6%;  Score 678;  DB 2;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-64;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy        135 DCWEPVQE 142
              ||||||||
Db        121 DCWEPVQE 128


RESULT 11
AAY53217
ID   AAY53217 standard; protein; 128 AA.
XX
AC   AAY53217;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human G-CSF mutant protein sequence SEQ ID NO:160.
XX
KW   Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
KW   colony stimulating factor; haematopoietic growth factor; lymphokine;
KW   fusion protein; haematopoietic disorder; infection; cancer;
```

KW radiation therapy; chemotherapy; bone marrow suppressive drug;
KW bone marrow activation; blood cell activation; blood transplant.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6022535-A.
XX
PD 08-FEB-2000.
XX
PF 06-JUN-1995; 95US-00469318.
XX
PR 04-FEB-1994; 94US-00192325.
PR 02-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Easton AM, Klein BK;
PI Paik K, Thomas JW, Mckearn JP, Olins PO, Caparon MH;
XX
DR WPI; 2000-160368/14.
XX
PT Treating hematopoietic disorders with fusion proteins comprising mutated
PT interleukin-3 fused with secondary colony stimulating factors or other
PT interleukin-3 variants.
XX
PS Example 20; Col 109-111; 276pp; English.
XX
CC Methods have been developed for treating haematopoietic disorders with
CC fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-
CC 3) variants or mutant proteins (muteins) fused with secondary colony
CC stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
CC and/or haematopoietic colony stimulating factors) or other interleukin-3
CC variants with or without a linker. The methods may be used in vivo to
CC treat haematopoietic disorders resulting from bacterial, viral and fungal
CC infections, cancer radiation therapy, chemotherapy or bone marrow
CC suppressive drugs. They may also be used in vitro to stimulate bone
CC marrow and blood cell activation and growth prior to infusion of the bone
CC marrow and blood transplants into patients. IL-3 is a haematopoietic
CC growth factor which has the property of being able to promote the
CC survival, growth and differentiation of haematopoietic cells. The fusion
CC molecules are characterised by possessing the usual activity of both of
CC their constituent peptides and further by having a biological or
CC physiological activity greater than the additive function of the IL-3 or
CC second CSF alone (i.e. the peptides act synergistically). Their activity
CC may also be further enhanced by the mutations they comprise. The
CC variations may further reduce undesirable side effects associated with IL
CC -3. AAY53130 to AAY53226, and AAA03721 to AAA03782 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 128 AA;

Query Match 88.6%; Score 678; DB 3; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy        135 DCWEPVQE 142
              ||||||||
Db        121 DCWEPVQE 128
```

RESULT 12
AAE14011
ID AAE14011 standard; protein; 128 AA.
XX
AC AAE14011;
XX
DT 26-FEB-2002 (first entry)
XX
DE Chemically modified myelopoietin (MPO) conjugate related protein #11.
XX
KW Myelopoietin conjugate; MPO; immunosuppressive; vulnerary; antiparasitic;
KW antibacterial; virucide; interleukin-3; IL-3; haematopoietic disorder;
KW haematopoietic growth factor receptor; neutropenia; thrombocytopenia;
KW leukopenia; anaemia; chemotherapy; bone marrow transplantation; burn;
KW radiation therapy; haematopoietic progenitor mobilisation; infection;
KW wound healing.
XX
OS Unidentified.
XX
PN WO200176639-A2.
XX
PD 18-OCT-2001.
XX
PF 06-APR-2001; 2001WO-US011256.
XX
PR 06-APR-2000; 2000US-0195496P.
XX
PA (PHAA) PHARMACIA CORP.
PA (FINN/) FINN R.
PA (GOKA/) GOKARN Y.
PA (HILL/) HILLS R.
PA (NICA/) NICASTRO P.
PA (QIHH/) QI H.
PA (SEDO/) SEDO K.
PA (SIEG/) SIEGEL N.
PA (WALT/) WALTER S.
XX
PI Finn R, Gokarn Y, Hills R, Nicastro P, Qi H, Sedo K, Siegel N;
PI Walter S;
XX
DR WPI; 2001-657130/75.
XX
PT Myelopoietin conjugate for treating e.g. leukopenia comprises a water-
PT soluble polymer attached to the protein.
XX
PS Disclosure; Page 215; 429pp; English.
XX
CC The invention relates to chemically modified myelopoietin (MPO)
CC conjugates having at least one water-soluble polymer molecule covalently
CC attached, via activating group, to at least one amino acid residue of a
CC biologically active myelopoietin polypeptide. MPOs are multifunctional
CC agonists of human interleukin-3 (IL-3) and another haematopoietic growth
CC factor receptor. Sequences of the invention are useful for treating
CC haematopoietic disorders (e.g. neutropenia, leukopenia, thrombocytopenia
CC and anaemia), including those arising from chemotherapy and radiation
CC therapy. MPOs are also useful in bone marrow transplantation, wound
CC healing, burn treatment and the treatment of parasite, bacterial or viral
CC infection. They are useful for mobilising haematopoietic progenitors and
CC stem cells. The chemically modified MPOs have a longer lasting neutrophil
CC -releasing activity, decreased clearance rate, increased stability and
CC decreased antigenicity than unmodified myelopoietins. The present
CC sequence is a chemically modified myelopoietin conjugate related protein
XX
SQ Sequence 128 AA;

Query Match 88.6%; Score 678; DB 4; Length 128;
Best Local Similarity 100.0%; Pred. No. 2.3e-64;
Matches 128; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120
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Qy        135 DCWEPVQE 142
              ||||||||
Db        121 DCWEPVQE 128
```

RESULT 13
ABG97784
ID ABG97784 standard; protein; 128 AA.
XX
AC ABG97784;
XX
DT 18-DEC-2002 (first entry)
XX
DE Human Interleukin-3 chimaeric protein #39.
XX
KW Human; interleukin-3; IL-3; mutant; mutein; stem cell;
KW haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; G-CSF;
KW G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
KW human growth hormone; B-cell growth factor; leukaemia;
KW B-cell differentiation factor; eosinophil differentiation factor;
KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
KW myelofibrosis.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN US6436387-B1.
XX
PD 20-AUG-2002.
XX
PF 09-DEC-1996; 96US-00762227.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 04-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2002-749206/81.
XX
PT Ex vivo expansion of stem cells, for enhancing transduction efficiency of
PT cultured stem cells, comprises culturing stem cells in growth medium
PT having mutant interleukin-3, and hematopoietic factor, and harvesting
PT cultured cells.
XX
PS Claim 8; Col 283-284; 203pp; English.
XX
CC The invention relates to ex vivo expansion of stem cells, comprises
CC culturing stem cells with a growth medium comprising a chimaera protein,
CC and harvesting the cultured stem cells. The chimaera is based on a
CC mutated human interleukin-3 (IL_3) sequence coupled to a haematopoietic
CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
CC CSFSer17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
CC differentiation factor, eosinophil differentiation factor and stem cell
CC factor (SCF)) via a peptide linker. The formula for the chimaera is given
CC in the specification. Also included is a method for enhancing the
CC efficiency of the transduction of cultured stem cells by a heterologous
CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
CC culturing the stem cells with a growth medium comprising the chimaera (c)
CC transducing DNA into cultured cells; and (d) harvesting the transduced
CC cells. The method is useful for ex vivo expansion of stem cells, and
CC enhancing the efficiency of the transduction of cultured stem cells by a
CC heterologous gene. The method is also useful for treating a patient
CC having a haematopoietic disorder. The expanded haematopoietic cells are
CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
CC and myelofibrosis. The present sequence is a human IL-3
CC mutant/haematopoietic factor chimaeric sequence
XX
SQ Sequence 128 AA;

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  Query Match             88.6%;  Score 678;  DB 5;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-64;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy        135 DCWEPVQE 142
              ||||||||
Db        121 DCWEPVQE 128
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RESULT 14
ADJ14372
ID ADJ14372 standard; protein; 128 AA.
XX
AC ADJ14372;
XX
DT 20-MAY-2004 (first entry)
XX
DE Protein related to human interleukin-3 (IL-3) mutant protein SEQ ID 140.
XX
KW stem cell; antianaemic; immunostimulant; immunomodulator;
KW antiinflammatory; dermatological; immunosuppressive; cytostatic;
KW neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;
KW lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
KW Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
KW myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3.
XX
OS Unidentified.
XX
PN US2003185790-A1.
XX
PD 02-OCT-2003.
XX
PF 26-FEB-2002; 2002US-00083446.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 02-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
PR 09-DEC-1996; 96US-00762227.
XX
PA (BAUE/) BAUER S C.
PA (ABRA/) ABRAMS M A.
PA (BRAF/) BRAFORD-GOLDBERG S R.
PA (CAPA/) CAPARON M H.
PA (EAST/) EASTON A M.
PA (KLEI/) KLEIN B K.
PA (MCKE/) MCKEARN J P.
PA (OLIN/) OLINS P O.
PA (PAIK/) PAIK K.
PA (THOM/) THOMAS J W.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX

```
DR   WPI; 2004-096775/10.
XX
PT   Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating
PT   aplastic anemia, involves culturing the stem cells with growth medium
PT   comprising chimera protein, and harvesting the cultured stem cells.
XX
PS   Disclosure; SEQ ID NO 160; 202pp; English.
XX
CC   The invention relates to a novel method whereby stem cells are ex vivo
CC   expanded via culturing the stem cells with a growth medium comprising a
CC   chimera protein, followed by harvesting of the cultured stem cells. The
CC   method of the invention has antianaemic, immunostimulant,
CC   immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC   cytostatic and neuroprotective applications and may be useful to target
CC   haemopoietic cells for gene therapy, preferably for treating patients
CC   having a haemopoietic disorder characterised by decreased levels of
CC   myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC   system. The expanded ex vivo cells may be used to treat neutropenia,
CC   aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC   systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC   myelofibrosis. The current sequence is that of a protein related to the
CC   human interleukin-3 (IL-3) mutant protein of the invention.
XX
SQ   Sequence 128 AA;

  Query Match             88.6%;  Score 678;  DB 8;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-64;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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Qy        135 DCWEPVQE 142
              ||||||||
Db        121 DCWEPVQE 128


RESULT 15
AAR79320
ID   AAR79320 standard; protein; 274 AA.
XX
AC   AAR79320;
XX
DT   25-AUG-1999  (first entry)
XX
DE   IL-3 containing fusion protein.
XX
KW   interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW   mutant; mutein; fusion protein.
XX
OS   Synthetic.
XX
PN   WO9521254-A1.
XX
PD   10-AUG-1995.
XX
PF   02-FEB-1995;   95WO-US001185.
XX
PR   04-FEB-1994;   94US-00192325.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer CS,  Abrams MA,  Braford-Goldberg SR,  Caparon MH,  Easton AM;
PI   Klein BK,  Mckearn JP,  Olins PO,  Paik K,  Thomas JW;
XX
DR   WPI; 1995-283774/37.
DR   N-PSDB; AAQ97183.
XX
PT   Fusion proteins comprising a human interleukin-3 variant, a linker and
PT   interleukin-3, a variant or a colony stimulating factor - useful to
PT   increase haematopoietic cell prodn. in a mammal.
XX
PS   Claim 16; Page 87-88; 447pp; English.
XX
CC   A new fusion protein has the formula R1-L-R2, R2-L-R1, R1-R2, R2-R1, R1-L
CC   -R1 or R1-R1, in which R1 is a mutant or variant of human interleukin-3
CC   (hIL-3) having the present generic sequence, R2 is a second colony
CC   stimulating factor (CSF) including cytokine, lymphokine, interleukin,
CC   haematopoietic growth factor or IL-3 variant, and L is a linker. The
CC   present sequence corresponds to native hIL-3(1-133) in which 1-14 amino
CC   acids may be deleted from the N-terminal, 1-15 amino acids can be deleted
CC   from the C-terminal, and at least 4 and up to 44 amino acids in the
CC   region 17-123 are different from those in the native protein. The fusion
CC   protein is used to increase haematopoietic cell production. It is also
CC   useful as an IL-3 antagonist or as a discrete antigenic fragment for
CC   production of antibodies useful in immunoassays and immunotherapy.
CC   Antagonists are used to block the growth of certain cancer cells and in
CC   treatment of asthma. The fusion protein can also be used to stimulate
CC   bone marrow and blood cell activation and growth in vitro before infusion
CC   ; and to treat diseases characterised by decreased levels of myeloid,
CC   erythroid, lymphoid and/or megakaryocyte cells of the haematopoietic
CC   system. The protein has the usual activity of both its component
CC   proteins, but may have increased synergistic activity and reduced
CC   undesired side effects
XX
SQ   Sequence 274 AA;

  Query Match             88.6%;  Score 678;  DB 2;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 6.4e-64;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
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Db        147 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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Db        207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266

Qy        135 DCWEPVQE 142
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Db        267 DCWEPVQE 274


Search completed: March  8, 2005, 16:10:22
Job time : 167 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 8, 2005, 16:13:34 ; Search time 131 Seconds
(without alignments)
356.675 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	682	89.2	259	14	US-10-083-446-141	Sequence 141, App
2	678	88.6	128	14	US-10-083-446-160	Sequence 160, App
3	678	88.6	274	14	US-10-083-446-144	Sequence 144, App
4	678	88.6	301	14	US-10-083-446-142	Sequence 142, App
5	675	88.2	712	15	US-10-609-346-10	Sequence 10, Appl
6	673	88.0	127	9	US-09-821-883-18	Sequence 18, Appl
7	673	88.0	127	9	US-09-800-016-1	Sequence 1, Appli
8	673	88.0	127	9	US-09-792-793A-15	Sequence 15, Appl
9	673	88.0	127	14	US-10-400-377-8	Sequence 8, Appli
10	673	88.0	127	14	US-10-400-708-8	Sequence 8, Appli
11	673	88.0	127	14	US-10-298-148-8	Sequence 8, Appli
12	673	88.0	127	15	US-10-375-209A-15	Sequence 15, Appl
13	673	88.0	127	16	US-10-658-834A-202	Sequence 202, App
14	673	88.0	127	16	US-10-743-295-5	Sequence 5, Appli
15	673	88.0	127	16	US-10-773-939-8	Sequence 8, Appli
16	673	88.0	127	16	US-10-774-149-8	Sequence 8, Appli
17	673	88.0	143	15	US-10-449-831A-142	Sequence 142, App
18	673	88.0	144	9	US-09-923-246-114	Sequence 114, App
19	673	88.0	144	14	US-10-295-723-114	Sequence 114, App
20	673	88.0	144	14	US-10-282-622-10	Sequence 10, Appl
21	673	88.0	144	14	US-10-131-985-15	Sequence 15, Appl
22	673	88.0	144	15	US-10-116-275-217	Sequence 217, App
23	673	88.0	144	15	US-10-456-780-10	Sequence 10, Appl
24	673	88.0	144	15	US-10-411-037-18	Sequence 18, Appl
25	673	88.0	144	15	US-10-609-346-20	Sequence 20, Appl
26	673	88.0	144	15	US-10-411-026-18	Sequence 18, Appl
27	673	88.0	144	15	US-10-447-315-19	Sequence 19, Appl
28	673	88.0	144	15	US-10-410-962-18	Sequence 18, Appl
29	673	88.0	144	15	US-10-411-049-18	Sequence 18, Appl
30	673	88.0	144	16	US-10-659-684-114	Sequence 114, App
31	673	88.0	144	16	US-10-410-930-18	Sequence 18, Appl
32	673	88.0	144	16	US-10-410-997-18	Sequence 18, Appl
33	673	88.0	144	16	US-10-411-012-18	Sequence 18, Appl
34	673	88.0	144	16	US-10-287-994-18	Sequence 18, Appl
35	673	88.0	144	16	US-10-659-295-27	Sequence 27, Appl
36	673	88.0	144	16	US-10-410-913-18	Sequence 18, Appl
37	673	88.0	144	16	US-10-666-122-3	Sequence 3, Appli
38	673	88.0	144	16	US-10-666-122-5	Sequence 5, Appli
39	673	88.0	144	17	US-10-901-417-15	Sequence 15, Appl
40	673	88.0	144	17	US-10-410-980-18	Sequence 18, Appl
41	673	88.0	191	15	US-10-449-831A-188	Sequence 188, App
42	673	88.0	610	9	US-09-783-708-1	Sequence 1, Appli
43	673	88.0	690	9	US-09-821-883-2	Sequence 2, Appli
44	671	87.7	127	16	US-10-658-834A-376	Sequence 376, App
45	670	87.6	127	16	US-10-658-834A-362	Sequence 362, App

ALIGNMENTS

RESULT 1
US-10-083-446-141
; Sequence 141, Application US/10083446
; Publication No. US20030185790A1
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; Bauer, S. C.
; Braford-Goldberg, Sarah R.
; Caparon, Maire H.
; Easton, Alan M.
; Klein, Barbara K.
; McKearn, John P.
; Olins, Peter O.
; Paik, Kumnan
; Thomas, John W.
; TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
; Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
; Corporate Patent Dept., Mail Zone O4E
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/083,446
; FILING DATE: 26-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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;             APPLICATION NUMBER: 08/762,227
;             FILING DATE: 09-DEC-1996
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: S. Christopher Bauer
;             REGISTRATION NUMBER: 42,305
;             REFERENCE/DOCKET NUMBER: C-2790/6
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (636)737-6257
;             TELEFAX: (636)737-5452
;   INFORMATION FOR SEQ ID NO: 141:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 259 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-10-083-446-141

  Query Match             89.2%;  Score 682;  DB 14;  Length 259;
  Best Local Similarity   97.0%;  Pred. No. 7.2e-64;
  Matches  130;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
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Qy         69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
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Qy        129 LLVIPFDCWEPVQE 142
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Db        246 LLVIPFDCWEPVQE 259


RESULT 2
US-10-083-446-160
; Sequence 160, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Thomas, John W.
;        TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                            Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;        NUMBER OF SEQUENCES: 197
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                        Corporate Patent Dept., Mail Zone O4E
;             STREET: 800 N. Lindbergh
;             CITY: St. Louis
;             STATE: Missouri
;             COUNTRY: USA
;             ZIP: 63167
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/083,446
;             FILING DATE: 26-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/762,227
;             FILING DATE: 09-DEC-1996
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: S. Christopher Bauer
;             REGISTRATION NUMBER: 42,305
;             REFERENCE/DOCKET NUMBER: C-2790/6
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (636)737-6257
;             TELEFAX: (636)737-5452
;   INFORMATION FOR SEQ ID NO: 160:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 128 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-10-083-446-160

  Query Match             88.6%;  Score 678;  DB 14;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 7.5e-64;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
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Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy        135 DCWEPVQE 142
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Db        121 DCWEPVQE 128


RESULT 3
US-10-083-446-144
; Sequence 144, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Thomas, John W.
;        TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                            Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;        NUMBER OF SEQUENCES: 197
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                        Corporate Patent Dept., Mail Zone O4E
;             STREET: 800 N. Lindbergh
;             CITY: St. Louis
;             STATE: Missouri
;             COUNTRY: USA
;             ZIP: 63167
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
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;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/10/083,446
;               FILING DATE: 26-Feb-2002
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: 08/762,227
;               FILING DATE: 09-DEC-1996
;               APPLICATION NUMBER: US 08/192,325
;               FILING DATE: 14-FEB-1994
;               APPLICATION NUMBER: US 08/446,872
;               FILING DATE: 06-JUN-1995
;          ATTORNEY/AGENT INFORMATION:
;               NAME: S. Christopher Bauer
;               REGISTRATION NUMBER: 42,305
;               REFERENCE/DOCKET NUMBER: C-2790/6
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (636)737-6257
;               TELEFAX: (636)737-5452
;     INFORMATION FOR SEQ ID NO: 144:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 274 amino acids
;               TYPE: amino acid
;               STRANDEDNESS: <Unknown>
;               TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 144:
US-10-083-446-144

  Query Match            88.6%;  Score 678;  DB 14;  Length 274;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-63;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266

Qy        135 DCWEPVQE 142
              ||||||||
Db        267 DCWEPVQE 274


RESULT 4
US-10-083-446-142
; Sequence 142, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;          APPLICANT: Abrams, Mark A.
;                     Bauer, S. C.
;                     Braford-Goldberg, Sarah R.
;                     Caparon, Maire H.
;                     Easton, Alan M.
;                     Klein, Barbara K.
;                     McKearn, John P.
;                     Olins, Peter O.
;                     Paik, Kumnan
;                     Thomas, John W.
;          TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                              Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;          NUMBER OF SEQUENCES: 197
;          CORRESPONDENCE ADDRESS:
;               ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                          Corporate Patent Dept., Mail Zone O4E
;               STREET: 800 N. Lindbergh
;               CITY: St. Louis
;               STATE: Missouri
;               COUNTRY: USA
;               ZIP: 63167
;          COMPUTER READABLE FORM:
;               MEDIUM TYPE: Floppy disk
;               COMPUTER: IBM PC compatible
;               OPERATING SYSTEM: PC-DOS/MS-DOS
;               SOFTWARE: PatentIn Release #1.0, Version #1.25
;          CURRENT APPLICATION DATA:
;               APPLICATION NUMBER: US/10/083,446
;               FILING DATE: 26-Feb-2002
;               CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;               APPLICATION NUMBER: 08/762,227
;               FILING DATE: 09-DEC-1996
;               APPLICATION NUMBER: US 08/192,325
;               FILING DATE: 14-FEB-1994
;               APPLICATION NUMBER: US 08/446,872
;               FILING DATE: 06-JUN-1995
;          ATTORNEY/AGENT INFORMATION:
;               NAME: S. Christopher Bauer
;               REGISTRATION NUMBER: 42,305
;               REFERENCE/DOCKET NUMBER: C-2790/6
;          TELECOMMUNICATION INFORMATION:
;               TELEPHONE: (636)737-6257
;               TELEFAX: (636)737-5452
;     INFORMATION FOR SEQ ID NO: 142:
;          SEQUENCE CHARACTERISTICS:
;               LENGTH: 301 amino acids
;               TYPE: amino acid
;               STRANDEDNESS: <Unknown>
;               TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 142:
US-10-083-446-142

  Query Match            88.6%;  Score 678;  DB 14;  Length 301;
  Best Local Similarity  100.0%;  Pred. No. 2.3e-63;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 233

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 293

Qy        135 DCWEPVQE 142
              ||||||||
Db        294 DCWEPVQE 301


RESULT 5
US-10-609-346-10
; Sequence 10, Application US/10609346
; Publication No. US20040063635A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Zailin
;  APPLICANT:  Fu, Yan
;  TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLO
;  TITLE OF INVENTION:  EFFECTS
;  FILE REFERENCE: ZYU-0603
;  CURRENT APPLICATION NUMBER: US/10/609,346
;  CURRENT FILING DATE:  2003-06-26
;  PRIOR APPLICATION NUMBER: US 60/392,948
;  PRIOR FILING DATE: 2002-07-01
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
;   LENGTH: 712
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: HSA-GMCSF
US-10-609-346-10
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  Query Match             88.2%;  Score 675;  DB 15;  Length 712;
  Best Local Similarity   99.2%;  Pred. No. 1.5e-62;
  Matches  127;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        585 LAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 644

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        645 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 704

Qy        135 DCWEPVQE 142
              ||||||||
Db        705 DCWEPVQE 712


RESULT 6
US-09-821-883-18
; Sequence 18, Application US/09821883
; Patent No. US20020061310A1
; GENERAL INFORMATION:
;  APPLICANT: Laus, Reiner
;  APPLICANT:  Vidovic, Damir
;  APPLICANT:  Graddis, Thomas
;  TITLE OF INVENTION: Compositions and Methods for Dendritic
;  TITLE OF INVENTION:  Cell-Based Immunotherapy
;  FILE REFERENCE: 7636-0022.30
;  CURRENT APPLICATION NUMBER: US/09/821,883
;  CURRENT FILING DATE:  2001-03-30
;  PRIOR APPLICATION NUMBER: US 60/193,504
;  PRIOR FILING DATE: 2000-03-30
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-821-883-18

  Query Match             88.0%;  Score 673;  DB 9;  Length 127;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127


RESULT 7
US-09-800-016-1
; Sequence 1, Application US/09800016
; Patent No. US20020141970A1
; GENERAL INFORMATION:
;  APPLICANT:  Pettit, Dean
;  APPLICANT:  Jochheim, Claudia
;  TITLE OF INVENTION:   STABLE AQUEOUS SOLUTIONS OF GRANULOCYTE MACROPHAGE COLONY-STIMU
;  TITLE OF INVENTION:  FACTOR
;  FILE REFERENCE:  3253
;  CURRENT APPLICATION NUMBER: US/09/800,016
;  CURRENT FILING DATE:  2001-03-05
;  NUMBER OF SEQ ID NOS:  1
;  SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 1
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-800-016-1

  Query Match             88.0%;  Score 673;  DB 9;  Length 127;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127


RESULT 8
US-09-792-793A-15
; Sequence 15, Application US/09792793A
; Patent No. US20020168370A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601D
;  CURRENT APPLICATION NUMBER: US/09/792,793A
;  CURRENT FILING DATE:  2001-02-22
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: homo sapien
;   FEATURE:
;   OTHER INFORMATION: Human Chemokine Polypeptide: GM-CSF
US-09-792-793A-15

  Query Match             88.0%;  Score 673;  DB 9;  Length 127;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127


RESULT 9
US-10-400-377-8
; Sequence 8, Application US/10400377
; Publication No. US20030162949A1
; GENERAL INFORMATION:
;  APPLICANT: Cox III, George N
;  APPLICANT:  Bolder Biotechnology, Inc.
;  TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
;  FILE REFERENCE: 4152-1-PUS
;  CURRENT APPLICATION NUMBER: US/10/400,377
;  CURRENT FILING DATE:  2003-03-26
;  PRIOR APPLICATION NUMBER: US/09/462,941
;  PRIOR FILING DATE: 2000-01-14
```

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;  PRIOR APPLICATION NUMBER: 60/052,516
;  PRIOR FILING DATE: 1997-07-14
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-400-377-8

  Query Match            88.0%;  Score 673;  DB 14;  Length 127;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127


RESULT 10
US-10-400-708-8
; Sequence 8, Application US/10400708
; Publication No. US20030166865A1
; GENERAL INFORMATION:
;  APPLICANT: Cox III, George N
;  APPLICANT:  Bolder Biotechnology, Inc.
;  TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
;  FILE REFERENCE: 4152-1-PUS
;  CURRENT APPLICATION NUMBER: US/10/400,708
;  CURRENT FILING DATE:  2003-03-26
;  PRIOR APPLICATION NUMBER: US/09/462,941
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/052,516
;  PRIOR FILING DATE: 1997-07-14
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-400-708-8

  Query Match            88.0%;  Score 673;  DB 14;  Length 127;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127


RESULT 11
US-10-298-148-8
; Sequence 8, Application US/10298148
; Publication No. US20030171284A1
; GENERAL INFORMATION:
;  APPLICANT: Cox III, George N
;  APPLICANT:  Bolder Biotechnology, Inc.
;  TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
;  FILE REFERENCE: 4152-1-PUS
;  CURRENT APPLICATION NUMBER: US/10/298,148
;  CURRENT FILING DATE:  2002-11-15
;  PRIOR APPLICATION NUMBER: US/09/462,941
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/052,516
;  PRIOR FILING DATE: 1997-07-14
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-298-148-8

  Query Match            88.0%;  Score 673;  DB 14;  Length 127;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127


RESULT 12
US-10-375-209A-15
; Sequence 15, Application US/10375209A
; Publication No. US20030215421A1
; GENERAL INFORMATION:
;  APPLICANT: McDonald, John R.
;  APPLICANT:  Coggins, Philip
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
;  TITLE OF INVENTION:  OTHER INFLAMMATORY CONDITIONS AND DISORDERS
;  FILE REFERENCE: 25020-601E
;  CURRENT APPLICATION NUMBER: US/10/375,209A
;  CURRENT FILING DATE:  2003-02-24
;  NUMBER OF SEQ ID NOS: 93
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: homo sapien
;   FEATURE:
;   OTHER INFORMATION: Human Chemokine Polypeptide: GM-CSF
US-10-375-209A-15

  Query Match            88.0%;  Score 673;  DB 15;  Length 127;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127
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```
RESULT 13
US-10-658-834A-202
; Sequence 202, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
;  APPLICANT: Gantier, Rene
;  APPLICANT:  Guyon, Thierry
;  APPLICANT:  Drittanti, Lila
;  APPLICANT:  Vega, Manuel
;  TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
;  TITLE OF INVENTION:  Acid
;  TITLE OF INVENTION:  Molecules and Related Applications
;  FILE REFERENCE: 38751-922
;  CURRENT APPLICATION NUMBER: US/10/658,834A
;  CURRENT FILING DATE:  2003-09-08
;  PRIOR APPLICATION NUMBER: 60/457,135
;  PRIOR FILING DATE: 2003-03-21
;  PRIOR APPLICATION NUMBER: 60/409,898
;  PRIOR FILING DATE: 2002-09-09
;  NUMBER OF SEQ ID NOS: 1306
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 202
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;   DATABASE ACCESSION NUMBER: Genbank AAA98768
;   DATABASE ENTRY DATE: 1996-05-02
US-10-658-834A-202

  Query Match             88.0%;  Score 673;  DB 16;  Length 127;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127


RESULT 14
US-10-743-295-5
; Sequence 5, Application US/10743295
; Publication No. US20040136952A1
; GENERAL INFORMATION:
;    - -
;  APPLICANT: Bhaskaran, Shyam S.
;  APPLICANT:  Sherman, Merry R.
;  APPLICANT:  Saifer, Mark G.P.
;  APPLICANT:  Williams, L. David
;  TITLE OF INVENTION: POLYMER CONJUGATES OF CYTOKINES, CHEMOKINES, GROWTH FACTORS, POLY
;  TITLE OF INVENTION:  HORMONES AND ANTAGONISTS THEREOF WITH PRESERVED RECEPTOR-BINDING
;  TITLE OF INVENTION:  ACTIVITY
;  FILE REFERENCE: 2057.0060002/JAG/BJD
;  CURRENT APPLICATION NUMBER: US/10/743,295
;  CURRENT FILING DATE:  2003-12-23
;  PRIOR APPLICATION NUMBER: 60/479,914
;  PRIOR FILING DATE: 2003-06-20
;  PRIOR APPLICATION NUMBER: 60/436,020
;  PRIOR FILING DATE: 2002-12-26
;  NUMBER OF SEQ ID NOS: 9
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-743-295-5

  Query Match             88.0%;  Score 673;  DB 16;  Length 127;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
              |||||||
Db        121 CWEPVQE 127


RESULT 15
US-10-773-939-8
; Sequence 8, Application US/10773939
; Publication No. US20040175356A1
; GENERAL INFORMATION:
;  APPLICANT: Cox III, George N
;  APPLICANT:  Bolder Biotechnology, Inc.
;  TITLE OF INVENTION: Derivatives of Growth Hormone and Related Proteins
;  FILE REFERENCE: 4152-1-PUS
;  CURRENT APPLICATION NUMBER: US/10/773,939
;  CURRENT FILING DATE:  2004-02-05
;  PRIOR APPLICATION NUMBER: US/10/400,377
;  PRIOR FILING DATE: 2003-03-26
;  PRIOR APPLICATION NUMBER: US/09/462,941
;  PRIOR FILING DATE: 2000-01-14
;  PRIOR APPLICATION NUMBER: 60/052,516
;  PRIOR FILING DATE: 1997-07-14
;  NUMBER OF SEQ ID NOS: 41
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 127
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-773-939-8

  Query Match             88.0%;  Score 673;  DB 16;  Length 127;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-63;
  Matches  127;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         16 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 75
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Db          1 APARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE 60

Qy         76 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPFD 120

Qy        136 CWEPVQE 142
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Db        121 CWEPVQE 127


Search completed: March  8, 2005, 16:26:00
Job time : 132 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: March 8, 2005, 16:05:14 ; Search time 42 Seconds
(without alignments)
252.385 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHHHSSGIEGRMAPARS.....ENLKDFLLVIPFDCWEPVQE 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	682	89.2	259	3	US-08-469-318-141	Sequence 141, App
2	682	89.2	259	3	US-08-468-609A-141	Sequence 141, App
3	682	89.2	259	3	US-08-446-872A-141	Sequence 141, App
4	682	89.2	259	4	US-08-762-227A-141	Sequence 141, App
5	682	89.2	259	5	PCT-US95-01185-141	Sequence 141, App
6	678	88.6	128	3	US-08-469-318-160	Sequence 160, App
7	678	88.6	128	3	US-08-468-609A-160	Sequence 160, App
8	678	88.6	128	3	US-08-446-872A-160	Sequence 160, App
9	678	88.6	128	4	US-08-762-227A-160	Sequence 160, App
10	678	88.6	128	5	PCT-US95-01185-160	Sequence 160, App
11	678	88.6	274	3	US-08-469-318-144	Sequence 144, App
12	678	88.6	274	3	US-08-468-609A-144	Sequence 144, App
13	678	88.6	274	3	US-08-446-872A-144	Sequence 144, App
14	678	88.6	274	4	US-08-762-227A-144	Sequence 144, App
15	678	88.6	274	5	PCT-US95-01185-144	Sequence 144, App
16	678	88.6	301	3	US-08-469-318-142	Sequence 142, App
17	678	88.6	301	3	US-08-468-609A-142	Sequence 142, App
18	678	88.6	301	3	US-08-446-872A-142	Sequence 142, App
19	678	88.6	301	4	US-08-762-227A-142	Sequence 142, App
20	678	88.6	301	5	PCT-US95-01185-142	Sequence 142, App
21	673	88.0	127	1	US-08-318-193-2	Sequence 2, Appli
22	673	88.0	127	4	US-09-462-941-8	Sequence 8, Appli
23	673	88.0	127	6	5229496-15	Patent No. 5229496
24	673	88.0	127	6	5229496-15	Patent No. 5229496
25	673	88.0	131	6	5229496-2	Patent No. 5229496
26	673	88.0	131	6	5229496-2	Patent No. 5229496
27	673	88.0	144	1	US-08-284-393B-11	Sequence 11, Appl
28	673	88.0	144	3	US-09-522-217-114	Sequence 114, App
29	673	88.0	144	4	US-09-923-246-114	Sequence 114, App
30	673	88.0	144	4	US-10-295-723-114	Sequence 114, App
31	673	88.0	144	5	PCT-US95-08950-11	Sequence 11, Appl
32	673	88.0	165	1	US-08-318-193-8	Sequence 8, Appli
33	673	88.0	168	1	US-08-318-193-10	Sequence 10, Appl
34	673	88.0	515	2	US-09-146-283-2	Sequence 2, Appli
35	673	88.0	515	3	US-08-579-823A-2	Sequence 2, Appli
36	673	88.0	515	3	US-09-344-195-2	Sequence 2, Appli
37	673	88.0	782	2	US-09-146-283-4	Sequence 4, Appli
38	673	88.0	782	3	US-08-579-823A-4	Sequence 4, Appli
39	673	88.0	782	3	US-09-344-195-4	Sequence 4, Appli
40	669	87.5	127	6	5405952-2	Patent No. 5405952
41	669	87.5	127	6	5405952-2	Patent No. 5405952
42	668	87.3	127	1	US-08-225-224-4	Sequence 4, Appli
43	668	87.3	127	3	US-08-722-258-4	Sequence 4, Appli
44	668	87.3	127	5	PCT-US95-04468-4	Sequence 4, Appli
45	668	87.3	144	3	US-08-759-628-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-469-318-141
; Sequence 141, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 259 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-469-318-141

Query Match 89.2%; Score 682; DB 3; Length 259;
Best Local Similarity 97.0%; Pred. No. 1e-69;
Matches 130; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
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Db        126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy         69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy        129 LLVIPFDCWEPVQE 142
              ||||||||||||||
Db        246 LLVIPFDCWEPVQE 259
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RESULT 2
US-08-468-609A-141
; Sequence 141, Application US/08468609A

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; Patent No. 6030812
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,609A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  141:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  259 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-468-609A-141

  Query Match             89.2%;  Score 682;  DB 3;  Length 259;
  Best Local Similarity   97.0%;  Pred. No. 1e-69;
  Matches  130;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
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Db        126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy         69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy        129 LLVIPFDCWEPVQE 142
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Db        246 LLVIPFDCWEPVQE 259


RESULT 3
US-08-446-872A-141
; Sequence 141, Application US/08446872A
; Patent No. 6361977
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis
;    TITLE OF INVENTION:  Fusion Protein
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,872A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  141:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  259 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-446-872A-141

  Query Match             89.2%;  Score 682;  DB 3;  Length 259;
  Best Local Similarity   97.0%;  Pred. No. 1e-69;
  Matches  130;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
              ||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy         69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy        129 LLVIPFDCWEPVQE 142
              ||||||||||||||
Db        246 LLVIPFDCWEPVQE 259


RESULT 4
US-08-762-227A-141
; Sequence 141, Application US/08762227A
; Patent No. 6436387
;  GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
```

```
;                 Caparon, Maire H.
;                 Easton, Alan M.
;                 Klein, Barbara K.
;                 McKearn, John P.
;                 Olins, Peter O.
;                 Paik, Kumnan
;                 Thomas, John W.
;       TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
;                           Fusion Protein
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
;                       Corporate Patent Dept.
;            STREET: P. O. Box 5110
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60680
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/762,227A
;            FILING DATE: 09-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/192,325
;            FILING DATE: 14-FEB-1994
;            APPLICATION NUMBER: US 08/446,872
;            FILING DATE: 06-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bennett, Dennis A.
;            REGISTRATION NUMBER: 34,547
;            REFERENCE/DOCKET NUMBER: C-2790/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (708)470-6501
;            TELEFAX: (708)470-6881
;   INFORMATION FOR SEQ ID NO: 141:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 259 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-08-762-227A-141

  Query Match             89.2%;  Score 682;  DB 4;  Length 259;
  Best Local Similarity   97.0%;  Pred. No. 1e-69;
  Matches  130;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
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Db        126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy         69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy        129 LLVIPFDCWEPVQE 142
              ||||||||||||||
Db        246 LLVIPFDCWEPVQE 259


RESULT 5
PCT-US95-01185-141
; Sequence 141, Application PC/TUS9501185
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01185
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192325
;      FILING DATE:  14-FEB-1994
;  INFORMATION FOR SEQ ID NO:  141:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  259 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01185-141

  Query Match             89.2%;  Score 682;  DB 5;  Length 259;
  Best Local Similarity   97.0%;  Pred. No. 1e-69;
  Matches  130;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 SGIEGRMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 68
              ||    ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 SGGGSNMAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPT 185

Qy         69 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDF 245

Qy        129 LLVIPFDCWEPVQE 142
              ||||||||||||||
Db        246 LLVIPFDCWEPVQE 259


RESULT 6
US-08-469-318-160
; Sequence 160, Application US/08469318
; Patent No. 6022535
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,318
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/446,872
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  160:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-469-318-160

  Query Match             88.6%;  Score 678;  DB 3;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
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Db           1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy          75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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Db          61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy         135 DCWEPVQE 142
               ||||||||
Db         121 DCWEPVQE 128


RESULT 7
US-08-468-609A-160
; Sequence 160, Application US/08468609A
; Patent No. 6030812
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,609A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  160:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-468-609A-160

  Query Match             88.6%;  Score 678;  DB 3;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy          75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy         135 DCWEPVQE 142
               ||||||||
Db         121 DCWEPVQE 128


RESULT 8
US-08-446-872A-160
; Sequence 160, Application US/08446872A
; Patent No. 6361977
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis
;    TITLE OF INVENTION:  Fusion Protein
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,872A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  160:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-446-872A-160

  Query Match             88.6%;  Score 678;  DB 3;  Length 128;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy          75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy        135 DCWEPVQE 142
                ||||||||
Db        121 DCWEPVQE 128


RESULT 9
US-08-762-227A-160
; Sequence 160, Application US/08762227A
; Patent No. 6436387
;  GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
;                  Caparon, Maire H.
;                  Easton, Alan M.
;                  Klein, Barbara K.
;                  McKearn, John P.
;                  Olins, Peter O.
;                  Paik, Kumnan
;                  Thomas, John W.
;       TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
;                           Fusion Protein
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
;                       Corporate Patent Dept.
;            STREET: P. O. Box 5110
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60680
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/762,227A
;            FILING DATE: 09-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/192,325
;            FILING DATE: 14-FEB-1994
;            APPLICATION NUMBER: US 08/446,872
;            FILING DATE: 06-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bennett, Dennis A.
;            REGISTRATION NUMBER: 34,547
;            REFERENCE/DOCKET NUMBER: C-2790/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (708)470-6501
;            TELEFAX: (708)470-6881
;  INFORMATION FOR SEQ ID NO: 160:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 128 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: <Unknown>
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 160:
US-08-762-227A-160

  Query Match            88.6%;  Score 678;  DB 4;  Length 128;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy        135 DCWEPVQE 142
                ||||||||
Db        121 DCWEPVQE 128


RESULT 10
PCT-US95-01185-160
; Sequence 160, Application PC/TUS9501185
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01185
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192325
;      FILING DATE:  14-FEB-1994
;  INFORMATION FOR SEQ ID NO:  160:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  128 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01185-160

  Query Match            88.6%;  Score 678;  DB 5;  Length 128;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 60

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 120

Qy        135 DCWEPVQE 142
                ||||||||
Db        121 DCWEPVQE 128


RESULT 11
US-08-469-318-144
; Sequence 144, Application US/08469318
; Patent No. 6022535
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,318
;      FILING DATE:
;      CLASSIFICATION:
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/446,872
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  144:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  274 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-469-318-144

  Query Match           88.6%;  Score 678;  DB 3;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266

Qy        135 DCWEPVQE 142
              ||||||||
Db        267 DCWEPVQE 274


RESULT 12
US-08-468-609A-144
; Sequence 144, Application US/08468609A
; Patent No. 6030812
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,609A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  144:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  274 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-468-609A-144

  Query Match           88.6%;  Score 678;  DB 3;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266

Qy        135 DCWEPVQE 142
              ||||||||
Db        267 DCWEPVQE 274


RESULT 13
US-08-446-872A-144
; Sequence 144, Application US/08446872A
; Patent No. 6361977
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis
;    TITLE OF INVENTION:  Fusion Protein
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,872A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  144:
;    SEQUENCE CHARACTERISTICS:
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;      LENGTH:  274 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-446-872A-144

  Query Match             88.6%;  Score 678;  DB 3;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266

Qy        135 DCWEPVQE 142
              ||||||||
Db        267 DCWEPVQE 274


RESULT 14
US-08-762-227A-144
; Sequence 144, Application US/08762227A
; Patent No. 6436387
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Thomas, John W.
;        TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
;                            Fusion Protein
;        NUMBER OF SEQUENCES: 197
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
;                        Corporate Patent Dept.
;             STREET: P. O. Box 5110
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60680
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/762,227A
;             FILING DATE: 09-Dec-1996
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bennett, Dennis A.
;             REGISTRATION NUMBER: 34,547
;             REFERENCE/DOCKET NUMBER: C-2790/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (708)470-6501
;             TELEFAX: (708)470-6881
;   INFORMATION FOR SEQ ID NO: 144:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 274 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;          MOLECULE TYPE: protein
;          SEQUENCE DESCRIPTION: SEQ ID NO: 144:
US-08-762-227A-144

  Query Match             88.6%;  Score 678;  DB 4;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266

Qy        135 DCWEPVQE 142
              ||||||||
Db        267 DCWEPVQE 274


RESULT 15
PCT-US95-01185-144
; Sequence 144, Application PC/TUS9501185
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01185
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192325
;      FILING DATE:  14-FEB-1994
;  INFORMATION FOR SEQ ID NO:  144:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  274 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US95-01185-144

  Query Match             88.6%;  Score 678;  DB 5;  Length 274;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-69;
  Matches  128;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         15 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRL 206

Qy         75 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 ELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIPF 266

Qy        135 DCWEPVQE 142
              ||||||||
Db        267 DCWEPVQE 274


Search completed: March  8, 2005, 16:14:58
Job time : 43 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 11, 2005, 10:03:16 ; Search time 2574 Seconds
(without alignments)
8621.791 Million cell updates/sec

Title: US-10-723-083-1
Perfect score: 458
Sequence: 1 cggcccgggatgcaccacca.....gctagcgtcgacgcatgccg 458

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	319.2	69.7	905	6	A20088	A20088 BamHI-HindI
2	319.2	69.7	905	6	AR363245	AR363245 Sequence
c 3	319.2	69.7	906	6	A20089	A20089 BamHI-HindI
4	319.2	69.7	909	6	I49839	I49839 Sequence 9
5	318.4	69.5	384	6	A20082	A20082 PstI-Hind I
c 6	318.4	69.5	392	6	A20083	A20083 PstI-Hind I
7	318.4	69.5	392	6	I49837	I49837 Sequence 1
8	318.4	69.5	896	6	A20086	A20086 BamHI-HindI
c 9	318.4	69.5	896	6	A20087	A20087 BamHI-HindI
10	318.4	69.5	896	6	AR363244	AR363244 Sequence
11	318.4	69.5	900	6	I49838	I49838 Sequence 7
12	315	68.8	386	6	AR363243	AR363243 Sequence
13	284.4	62.1	435	6	CQ834915	CQ834915 Sequence
14	283.6	61.9	777	6	AR202206	AR202206 Sequence
15	283.6	61.9	777	6	AR223208	AR223208 Sequence
16	283	61.8	402	6	AR202280	AR202280 Sequence
17	283	61.8	402	6	AR223282	AR223282 Sequence
18	281	61.4	822	6	AR202220	AR202220 Sequence
19	281	61.4	822	6	AR223222	AR223222 Sequence
20	281	61.4	903	6	AR202217	AR202217 Sequence
21	281	61.4	903	6	AR223219	AR223219 Sequence
22	277.6	60.6	415	6	A00367	A00367 Artificial
c 23	277.6	60.6	415	6	A00368	A00368 Artificial
24	277.6	60.6	415	6	A14305	A14305 GM-CSF gene
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26	276.8	60.4	756	6	CQ721607	CQ721607 Sequence
27	276.8	60.4	756	6	CQ803372	CQ803372 Sequence
28	276.8	60.4	763	6	E02287	E02287 DNA encodin
29	276.8	60.4	787	6	I08093	I08093 Sequence 1
30	276.8	60.4	787	6	I08094	I08094 Sequence 1
31	276.8	60.4	787	6	I08401	I08401 Sequence 1
32	276.8	60.4	787	6	I09140	I09140 Sequence 1
33	276.8	60.4	787	6	I09160	I09160 Sequence 21
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35	276.8	60.4	2385	6	AR082744	AR082744 Sequence
36	276.8	60.4	2385	6	AR099963	AR099963 Sequence
37	276.8	60.4	2385	6	AR143949	AR143949 Sequence
38	276.2	60.3	644	6	E01141	E01141 cDNA encodi
39	276.2	60.3	660	6	AR364645	AR364645 Sequence
40	276.2	60.3	661	6	AR363793	AR363793 Sequence
41	276.2	60.3	1011	6	AR447690	AR447690 Sequence
42	275.8	60.2	435	6	AR533388	AR533388 Sequence
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44	275.2	60.1	505	6	I08646	I08646 Sequence 3
45	275.2	60.1	505	9	HUMCSFGMB	M11734 Human granu

ALIGNMENTS

RESULT 1
A20088
LOCUS A20088 905 bp DNA linear PAT 18-AUG-1994
DEFINITION BamHI-HindIII fragment in vector pAEO.GMCSF.
ACCESSION A20088
VERSION A20088.1 GI:583268
KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 905)
AUTHORS Garvin,R.T. and Malek,L.T.
TITLE An expression system for the secretion of bioactive human granulocyte macrophage colony stimulating factor (GM-CSF) and other heterologous proteins from streptomyces
JOURNAL Patent: EP 0352707-A 21 31-JAN-1990;
Cangene Corporation
FEATURES Location/Qualifiers
source 1. .905
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
ORIGIN

Query Match 69.7%; Score 319.2; DB 6; Length 905;
Best Local Similarity 86.9%; Pred. No. 3.6e-38;
Matches 351; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy         35 CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGG 94
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Db        502 CCGCCTCCGGGGCGTCTGCAGCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG 561

Qy         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCG 154
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Db        562 AGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG 621

Qy        155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT 214
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Db        622 CCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGT 681

Qy        215 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA 274
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Db        682 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCA 741

Qy        275 AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGA 334
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Db        742 AGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGA 801

Qy        335 CCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCC 394
              | || |||||||||||||||||| ||||||   |||||||||||||| ||||||||||
Db        802 CGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCC 861

Qy        395 TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
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Db        862 TCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 905


RESULT 2
AR363245
LOCUS       AR363245                905 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 3 from patent US 5200327.
ACCESSION   AR363245
VERSION     AR363245.1  GI:34424298
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 905)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     Expression system for the secretion of bioactive human granulocyte
            macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from streptomyces
  JOURNAL   Patent: US 5200327-A 3 06-APR-1993;
FEATURES             Location/Qualifiers
     source          1. .905
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             69.7%;  Score 319.2;  DB 6;  Length 905;
  Best Local Similarity   86.9%;  Pred. No. 3.6e-38;
  Matches  351;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         35 CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGG 94
              ||| |  || ||        || || || ||    ||    ||||| |||||||||||||
Db        502 CCGCCTCCGGGGCGTCTGCAGCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG 561

Qy         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCG 154
              ||||||| |||||||||||||||||||| | || |||||||||| || ||||| ||||
Db        562 AGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG 621

Qy        155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT 214
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Db        622 CCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGT 681

Qy        215 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA 274
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Db        682 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCA 741

Qy        275 AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGA 334
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Db        742 AGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGA 801

Qy        335 CCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCC 394
              | || |||||||||||||||||| ||||||   |||||||||||||| ||||||||||
Db        802 CGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCC 861

Qy        395 TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||| ||||||||||||||||||||||||||||||
Db        862 TCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 905


RESULT 3
A20089/c
LOCUS       A20089                  906 bp    DNA     linear   PAT 18-AUG-1994
DEFINITION  BamHI-HindIII fragment in vector pAEO.GMCSF.
ACCESSION   A20089
VERSION     A20089.1  GI:578985
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     An expression system for the secretion of bioactive human
            granulocyte macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from streptomyces
  JOURNAL   Patent: EP 0352707-A 22 31-JAN-1990;
            Cangene Corporation
FEATURES             Location/Qualifiers
     source          1. .906
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             69.7%;  Score 319.2;  DB 6;  Length 906;
  Best Local Similarity   86.9%;  Pred. No. 3.6e-38;
  Matches  351;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         35 CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGG 94
              ||| |  || ||        || || || ||    ||    ||||| |||||||||||||
Db        408 CCGCCTCCGGGGCGTCTGCAGCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG 349

Qy         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCG 154
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Db        348 AGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG 289

Qy        155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT 214
              |||||||||||||||||||||||||||||||| ||||||||||   | |||||||| || |
Db        288 CCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGT 229

Qy        215 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA 274
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Db        228 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCA 169

Qy        275 AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGA 334
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Db        168 AGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGA 109

Qy        335 CCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCC 394
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Db        108 CGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCC 49

Qy        395 TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
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Db         48 TCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 5


RESULT 4
I49839
LOCUS       I49839                  909 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 9 from patent US 5641663.
ACCESSION   I49839
VERSION     I49839.1  GI:2472059
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 909)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     Expression system for the secretion of bioactive human granulocyte
            macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from steptomyces
  JOURNAL   Patent: US 5641663-A 9 24-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .909
                     /organism="unknown"
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           69.7%;  Score 319.2;  DB 6;  Length 909;
  Best Local Similarity  86.9%;  Pred. No. 3.6e-38;
  Matches  351;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         35 CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGG 94
              ||| |  || ||        || || || ||    ||    ||||| ||||||||||||||
Db        502 CCGCCTCCGGGGCGTCTGCAGCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG 561

Qy         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCG 154
              ||||||| ||||||||||||||||||||| | || |||||||||| || ||||| ||||
Db        562 AGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG 621

Qy        155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT 214
              |||||||||||||||||||||||||||||| ||||||||||  | |||||||| || |
Db        622 CCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGT 681

Qy        215 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA 274
              |||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db        682 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCA 741

Qy        275 AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGA 334
              |||| ||||| |||||||||||||||||||||||| ||||||||||| || || |||||||
Db        742 AGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGA 801

Qy        335 CCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCC 394
              | || ||||||||||||||||||| ||||||    |||||||||||||| ||||||||||
Db        802 CGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCC 861

Qy        395 TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
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Db        862 TCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 905


RESULT 5
A20082
LOCUS       A20082                   384 bp    DNA     linear   PAT 18-AUG-1994
DEFINITION  PstI-Hind III fragment encoding GM-CSF.
ACCESSION   A20082
VERSION     A20082.1  GI:583266
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     An expression system for the secretion of bioactive human
            granulocyte macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from streptomyces
  JOURNAL   Patent: EP 0352707-A 13 31-JAN-1990;
            Cangene Corporation
FEATURES             Location/Qualifiers
     source          1. .384
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ORIGIN

  Query Match           69.5%;  Score 318.4;  DB 6;  Length 384;
  Best Local Similarity  89.3%;  Pred. No. 5.7e-38;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
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Db          1 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 60

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
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Db         61 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 120

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
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Db        121 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 180

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
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Db        181 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 240

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
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Db        241 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 300

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| ||||||||||||||||||||| ||||||
Db        301 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 360

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
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Db        361 TGCTGGGAGCCGGTGCAGGAGTGA 384


RESULT 6
A20083/c
LOCUS       A20083                   392 bp    DNA     linear   PAT 18-AUG-1994
DEFINITION  PstI-Hind III fragment encoding GM-CSF.
ACCESSION   A20083
VERSION     A20083.1  GI:578981
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     An expression system for the secretion of bioactive human
            granulocyte macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from streptomyces
  JOURNAL   Patent: EP 0352707-A 14 31-JAN-1990;
            Cangene Corporation
FEATURES             Location/Qualifiers
     source          1. .392
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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ORIGIN

  Query Match           69.5%;  Score 318.4;  DB 6;  Length 392;
  Best Local Similarity  89.3%;  Pred. No. 5.6e-38;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
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Db        388 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 329

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
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Db        328 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 269

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
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Db        268 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 209

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
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Db        208 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 149

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
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Db        148 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 89

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| ||||||||||||||||||||| ||||||
Db         88 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 29

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
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Db         28 TGCTGGGAGCCGGTGCAGGAGTGA 5


RESULT 7
I49837
LOCUS       I49837                   392 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 1 from patent US 5641663.
ACCESSION   I49837
VERSION     I49837.1  GI:2472057
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 392)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     Expression system for the secretion of bioactive human granulocyte
            macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from steptomyces
  JOURNAL   Patent: US 5641663-A 1 24-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .392
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                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             69.5%;  Score 318.4;  DB 6;  Length 392;
  Best Local Similarity   89.3%;  Pred. No. 5.6e-38;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || ||    ||    ||||| |||||||||||||||||||| ||||||||||||
Db          5 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 64

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              ||||||||| | || |||||||||| || ||||| ||||||||||||||||||||||||
Db         65 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 124

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
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Db        125 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 184

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
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Db        185 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 244

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
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Db        245 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 304

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| ||||||||||||||||||||| ||||||
Db        305 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 364

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
              ||||||||||||||||||||||||
Db        365 TGCTGGGAGCCGGTGCAGGAGTGA 388


RESULT 8
A20086
LOCUS       A20086                   896 bp    DNA     linear   PAT 18-AUG-1994
DEFINITION  BamHI-HindIII fragment in vector pAPO.GMCSF.
ACCESSION   A20086
VERSION     A20086.1  GI:583267
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     An expression system for the secretion of bioactive human
            granulocyte macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from streptomyces
  JOURNAL   Patent: EP 0352707-A 19 31-JAN-1990;
            Cangene Corporation
FEATURES             Location/Qualifiers
     source          1. .896
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             69.5%;  Score 318.4;  DB 6;  Length 896;
  Best Local Similarity   89.3%;  Pred. No. 4.7e-38;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || ||    ||    ||||| |||||||||||||||||||| ||||||||||||
Db        513 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 572

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              ||||||||| | || |||||||||| || ||||| ||||||||||||||||||||||||
Db        573 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 632

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||| ||||||||||  | |||||||| || ||||||||||||||||||||||
Db        633 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 692

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||||||||||| ||||| ||||||||||||||||||||||| ||||| |||||||||
Db        693 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 752

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              ||||||||||||| |||||||||| || || |||||||| || ||||||||||||||||
Db        753 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 812

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| ||||||||||||||||||||| ||||||
Db        813 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 872

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
              ||||||||||||||||||||||||
Db        873 TGCTGGGAGCCGGTGCAGGAGTGA 896


RESULT 9
A20087/c
LOCUS       A20087                   896 bp    DNA     linear   PAT 18-AUG-1994
DEFINITION  BamHI-HindIII fragment in vector pAPO.GMCSF.
ACCESSION   A20087
VERSION     A20087.1  GI:578984
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     An expression system for the secretion of bioactive human
            granulocyte macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from streptomyces
  JOURNAL   Patent: EP 0352707-A 20 31-JAN-1990;
            Cangene Corporation
FEATURES             Location/Qualifiers
     source          1. .896
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             69.5%;  Score 318.4;  DB 6;  Length 896;
  Best Local Similarity   89.3%;  Pred. No. 4.7e-38;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || ||    ||    ||||| |||||||||||||||||||| ||||||||||||
```

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Db        388 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 329

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCCGAGATGAACGAGACCGTG 174
              ||||||||| | || |||||||||||| || ||||| ||||||||||||||||||||||||
Db        328 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 269

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||||| ||||||||||   | |||||||| || ||||||||||||||||||||||
Db        268 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 209

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||||||||||||| ||||| |||||||||||||||||||||| ||||| |||||||||
Db        208 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 149

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              |||||||||||||| |||||||||| || || |||||||| || ||||||||||||||||
Db        148 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 89

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| ||||||||||||||||||||||| ||||||
Db         88 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 29

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||||||||||||||
Db         28 TGCTGGGAGCCGGTGCAGGAGTGA 5


RESULT 10
AR363244
LOCUS       AR363244                 896 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 2 from patent US 5200327.
ACCESSION   AR363244
VERSION     AR363244.1  GI:34424297
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 896)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     Expression system for the secretion of bioactive human granulocyte
            macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from streptomyces
  JOURNAL   Patent: US 5200327-A 2 06-APR-1993;
FEATURES             Location/Qualifiers
     source          1. .896
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             69.5%;  Score 318.4;  DB 6;  Length 896;
  Best Local Similarity   89.3%;  Pred. No. 4.7e-38;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || ||    ||    ||||| |||||||||||||||||||| ||||||||||
Db        513 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 572

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              ||||||||| | || |||||||||||| || ||||| ||||||||||||||||||||||||
Db        573 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 632

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||||| ||||||||||   | |||||||| || ||||||||||||||||||||||
Db        633 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 692

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||||||||||||| ||||| |||||||||||||||||||||| ||||| |||||||||
Db        693 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 752

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              |||||||||||||| |||||||||| || || |||||||| || ||||||||||||||||
Db        753 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 812

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| ||||||||||||||||||||||| ||||||
Db        813 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 872

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||||||||||||||
Db        873 TGCTGGGAGCCGGTGCAGGAGTGA 896


RESULT 11
I49838
LOCUS       I49838                   900 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 7 from patent US 5641663.
ACCESSION   I49838
VERSION     I49838.1  GI:2472058
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 900)
  AUTHORS   Garvin,R.T. and Malek,L.T.
  TITLE     Expression system for the secretion of bioactive human granulocyte
            macrophage colony stimulating factor (GM-CSF) and other
            heterologous proteins from steptomyces
  JOURNAL   Patent: US 5641663-A 7 24-JUN-1997;
FEATURES             Location/Qualifiers
     source          1. .900
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             69.5%;  Score 318.4;  DB 6;  Length 900;
  Best Local Similarity   89.3%;  Pred. No. 4.7e-38;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || ||    ||    ||||| |||||||||||||||||||| ||||||||||
Db        513 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 572

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              ||||||||| | || |||||||||||| || ||||| ||||||||||||||||||||||||
Db        573 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 632

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||||| ||||||||||   | |||||||| || ||||||||||||||||||||||
Db        633 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 692

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||||||||||||| ||||| |||||||||||||||||||||| ||||| |||||||||
Db        693 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 752

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              |||||||||||||| |||||||||| || || |||||||| || ||||||||||||||||
Db        753 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 812

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| ||||||||||||||||||||||| ||||||
Db        813 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 872

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||||||||||||||
Db        873 TGCTGGGAGCCGGTGCAGGAGTGA 896


RESULT 12
AR363243
LOCUS       AR363243                 386 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 1 from patent US 5200327.
ACCESSION   AR363243
VERSION     AR363243.1  GI:34424296
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
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           Unclassified.
REFERENCE  1  (bases 1 to 386)
  AUTHORS  Garvin,R.T. and Malek,L.T.
  TITLE    Expression system for the secretion of bioactive human granulocyte
           macrophage colony stimulating factor (GM-CSF) and other
           heterologous proteins from streptomyces
  JOURNAL  Patent: US 5200327-A 1 06-APR-1993;
FEATURES             Location/Qualifiers
     source          1. .386
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           68.8%;  Score 315;  DB 6;  Length 386;
  Best Local Similarity   91.7%;  Pred. No. 1.8e-37;
  Matches  333;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy         76 CCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAAC 135
              ||||| |||||||||||||||||||| |||||||||||||||||||| | || ||||||
Db         24 CCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAAC 83

Qy        136 CTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTC 195
              ||||| || ||||| |||||||||||||||||||||||||||||||||||||| |||||||||
Db         84 CTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTC 143

Qy        196 GATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGC 255
              ||  | |||||||| || |||||||||||||||||||||||||||||||||| |||||
Db        144 GACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGG 203

Qy        256 GGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCAC 315
              |||||||||||||||||||| ||||| ||||||||||||||||||||| ||||||
Db        204 GGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCAC 263

Qy        316 TGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAG 375
              ||||| || || |||||||| || ||||||||||||||||||| ||||||   ||||||
Db        264 TGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAG 323

Qy        376 GAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              |||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Db        324 GAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAG 383

Qy        436 TGA 438
              |||
Db        384 TGA 386


RESULT 13
CQ834915
LOCUS       CQ834915                435 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 2 from Patent WO2004059556.
ACCESSION   CQ834915
VERSION     CQ834915.1  GI:50834452
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Raab,D., Graf,M., Notka,F. and Wagner,R.
  TITLE     Method and device for optimizing a nucleotide sequence for the
            purpose of expression of a protein
  JOURNAL   Patent: WO 2004059556-A 2 15-JUL-2004;
            Geneart GmbH (DE)
FEATURES             Location/Qualifiers
     source          1. .435
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           62.1%;  Score 284.4;  DB 6;  Length 435;
  Best Local Similarity   84.0%;  Pred. No. 6.1e-33;
  Matches  321;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || ||  | ||||| |||||   ||| ||||| ||||||||||||||| || ||||||
Db         52 GCCCCTGCCAGAAGCCCTAGCCCTAGCACACAGCCTTGGGAGCACGTGAATGCCATCCAG 111

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              |||||| | || || || |||||   | | || || ||||||||||||||||||||||||
Db        112 GAGGCCAGGAGACTGCTGAACCTGAGCAGAGATACAGCCGCCGAGATGAACGAGACCGTG 171

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||  |||||||||||| || |||||||| || ||||| |||||||| || |||
Db        172 GAGGTGATCAGCGAGATGTTCGACCTGCAGGAGCCTACATGCCTGCAGACCCGGCTGGAG 231

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||| ||||||||||  | |||   || |||||||| |||||||| || || ||||||
Db        232 CTGTATAAGCAGGGCCTGAGAGGCTCTCTGACCAAGCTGAAGGGCCCCCTGACAATGATG 291

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              ||   |||||||||||||||||||| || ||||| |||||   ||||||||||||||||
Db        292 GCCAGCCACTACAAGCAGCACTGCCCTCCTACCCCTGAGACAAGCTGCGCCACCCAGATC 351

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              |||||||||||||||||||||||||||||||||||| |||||||||| || ||||||| |||||
Db        352 ATCACCTTCGAGAGCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGAT 411

Qy        415 TGCTGGGAGCCGGTGCAGGAGT 436
              |||||||||| ||||||||||
Db        412 TGCTGGGAGCCCGTGCAGGAGT 433


RESULT 14
AR202206
LOCUS       AR202206                777 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 55 from patent US 6361977.
ACCESSION   AR202206
VERSION     AR202206.1  GI:20256745
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Bauer,S.Christopher., Abrams,M.Allen., Braford-Goldberg,S.Ruth.,
            Caparon,M.Helena., Easton,A.Michael., Klein,B.Kure., McKearn,J.P.,
            Olins,P.O., Paik,K. and Thomas,J.W.
  TITLE     Methods of using multivariant IL-3 hematopoiesis fusion protein
  JOURNAL   Patent: US 6361977-A 55 26-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           61.9%;  Score 283.6;  DB 6;  Length 777;
  Best Local Similarity   81.6%;  Pred. No. 7.1e-33;
  Matches  328;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
              || |||  ||    | |||||| || ||  ||||  |||||| ||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCCGCGACACCGCC 153
              || |||||||| ||||||||||||||  | ||||| |||||     | ||||| ||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
              || |||||||| || || || || ||||| || || ||||| || ||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
              ||||| |||||||||| |||||||||||||||||||| || ||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
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Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
              || ||||| || |||||||| |||||||| || || ||||| |||||||| |||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              || || || ||||| || |||||||||||||| || ||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777


RESULT 15
AR223208
LOCUS       AR223208                777 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 55 from patent US 6436387.
ACCESSION   AR223208
VERSION     AR223208.1  GI:23331216
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
            Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P.O., Paik,K. and
            Thomas,J.W.
  TITLE     Methods of ex-vivo expansion of hematopoietic cells using
            multivariant IL-3 hematopoiesis chimera proteins
  JOURNAL   Patent: US 6436387-A 55 20-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           61.9%;  Score 283.6;  DB 6;  Length 777;
  Best Local Similarity   81.6%;  Pred. No. 7.1e-33;
  Matches  328;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
              || |||  ||    |  |||||| || || ||   ||||  |||||| ||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
              || |||||||| || ||||||||||||||  | ||||| |||||     | ||||| ||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
              || |||||||| || || || || ||||| || || ||||| || ||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
              ||||| |||||||||| |||||||||||||||||||| || ||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
              |||||||| | |||||||||||   |||||||||||||||||||| || ||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
              || ||||| || |||||||| |||||||| || || ||||| |||||||| |||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              || || || ||||| || |||||||||||||| || ||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777


Search completed: March 11, 2005, 16:42:03
Job time : 2582 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 11, 2005, 15:26:31 ; Search time 145 Seconds
(without alignments)
5168.377 Million cell updates/sec

Title: US-10-723-083-1
Perfect score: 458
Sequence: 1 cggcccgggatgcaccacca.....gctagcgtcgacgcatgccg 458

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	319.2	69.7	905	6	5200327-3	Patent No. 5200327
2	319.2	69.7	905	6	5200327-3	Patent No. 5200327
3	319.2	69.7	909	1	US-08-318-193-9	Sequence 9, Appli
4	318.4	69.5	392	1	US-08-318-193-1	Sequence 1, Appli
5	318.4	69.5	896	6	5200327-2	Patent No. 5200327
6	318.4	69.5	896	6	5200327-2	Patent No. 5200327
7	318.4	69.5	900	1	US-08-318-193-7	Sequence 7, Appli
8	315	68.8	386	6	5200327-1	Patent No. 5200327
9	315	68.8	386	6	5200327-1	Patent No. 5200327
10	312.6	68.3	435	4	US-10-188-056-31	Sequence 31, Appl
11	311	67.9	435	4	US-10-188-056-33	Sequence 33, Appl
12	283.6	61.9	777	3	US-08-469-318-55	Sequence 55, Appl
13	283.6	61.9	777	3	US-08-468-609A-55	Sequence 55, Appl
14	283.6	61.9	777	3	US-08-446-872A-55	Sequence 55, Appl
15	283.6	61.9	777	3	US-08-762-227A-55	Sequence 55, Appl
16	283.6	61.9	777	5	PCT-US95-01185-55	Sequence 55, Appl
17	283	61.8	402	3	US-08-469-318-176	Sequence 176, App
18	283	61.8	402	3	US-08-468-609A-176	Sequence 176, App
19	283	61.8	402	3	US-08-446-872A-176	Sequence 176, App
20	283	61.8	402	3	US-08-762-227A-176	Sequence 176, App
21	283	61.8	402	5	PCT-US95-01185-176	Sequence 176, App
22	281	61.4	822	3	US-08-469-318-69	Sequence 69, Appl
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25	281	61.4	822	3	US-08-762-227A-69	Sequence 69, Appl
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27	281	61.4	903	3	US-08-469-318-66	Sequence 66, Appl
28	281	61.4	903	3	US-08-468-609A-66	Sequence 66, Appl
29	281	61.4	903	3	US-08-446-872A-66	Sequence 66, Appl
30	281	61.4	903	3	US-08-762-227A-66	Sequence 66, Appl
31	281	61.4	903	5	PCT-US95-01185-66	Sequence 66, Appl
32	276.8	60.4	2385	2	US-09-146-283-3	Sequence 3, Appli
33	276.8	60.4	2385	3	US-08-579-823A-3	Sequence 3, Appli
34	276.8	60.4	2385	3	US-09-344-195-3	Sequence 3, Appli
35	276.2	60.3	660	6	5391485-2	Patent No. 5391485
36	276.2	60.3	660	6	5391485-2	Patent No. 5391485
37	276.2	60.3	661	6	5229496-1	Patent No. 5229496
38	276.2	60.3	661	6	5229496-1	Patent No. 5229496
39	276.2	60.3	1011	4	US-09-976-594-275	Sequence 275, App
40	275.8	60.2	435	3	US-08-848-760B-8	Sequence 8, Appli
41	275.8	60.2	435	4	US-09-826-025-8	Sequence 8, Appli
42	275.2	60.1	756	4	US-09-016-434-1195	Sequence 1195, Ap
43	275.2	60.1	1318	3	US-09-310-842-3	Sequence 3, Appli
44	274.6	60.0	1011	2	US-08-750-128-12	Sequence 12, Appl
45	274.6	60.0	1588	2	US-09-146-283-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
5200327-3
;Patent No. 5200327
; APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
; TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
;STREPTOMYCES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/224,568
; FILING DATE: 26-JUL-1988
;SEQ ID NO:3:
; LENGTH: 905
5200327-3

Query Match 69.7%; Score 319.2; DB 6; Length 905;
Best Local Similarity 86.9%; Pred. No. 1e-60;
Matches 351; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy         35 CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGG 94
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Db        502 CCGCCTCCGGGGCGTCTGCAGCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG 561

Qy         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCG 154
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Db        562 AGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG 621

Qy        155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT 214
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Qy        215 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA 274
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Db        682 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCA 741

Qy        275 AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGA 334
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Db        742 AGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGA 801

Qy        335 CCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCC 394
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Qy        395 TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
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Db        862 TCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 905
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RESULT 2

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5200327-3
;Patent No. 5200327
;    APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
;    TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
;STREPTOMYCES
;    NUMBER OF SEQUENCES: 24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/224,568
;      FILING DATE: 26-JUL-1988
;SEQ ID NO:3:
;      LENGTH: 905
5200327-3

  Query Match            69.7%;  Score 319.2;  DB 6;  Length 905;
  Best Local Similarity  86.9%;  Pred. No. 1e-60;
  Matches  351;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         35 CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGG 94
              ||| |  || ||        || || || ||    ||    ||||| ||||||||||||
Db        502 CCGCCTCCGGGGCGTCTGCAGCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG 561

Qy         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCG 154
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Db        562 AGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG 621

Qy        155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT 214
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Db        622 CCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGT 681

Qy        215 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA 274
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Qy        275 AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGA 334
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Db        742 AGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGA 801

Qy        335 CCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCC 394
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Db        802 CGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCC 861

Qy        395 TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
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Db        862 TCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 905


RESULT 3
US-08-318-193-9
; Sequence 9, Application US/08318193
; Patent No. 5641663
;  GENERAL INFORMATION:
;    APPLICANT:  GARVIN, Robert T.
;    APPLICANT:  MALEK, Lawrence T.
;    TITLE OF INVENTION:  AN EXPRESSION SYSTEM FOR THE SECRETION
;    TITLE OF INVENTION:  OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
;    TITLE OF INVENTION:  STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
;    TITLE OF INVENTION:  PROTEINS FROM STREPTOMYCES
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,193
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,314
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/224,568
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  18740/116 CACO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  909 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA oligonucleotide
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  399..902
US-08-318-193-9

  Query Match            69.7%;  Score 319.2;  DB 1;  Length 909;
  Best Local Similarity  86.9%;  Pred. No. 1e-60;
  Matches  351;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         35 CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGG 94
              ||| |  || ||        || || || ||    ||    ||||| ||||||||||||
Db        502 CCGCCTCCGGGGCGTCTGCAGCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG 561

Qy         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCG 154
              ||||||| |||||||||||||||||||| | || |||||||||| || ||||| ||||
Db        562 AGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG 621

Qy        155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT 214
              |||||||||||||||||||||||||||||||| |||||||||| | |||||||| || |
Db        622 CCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGT 681

Qy        215 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA 274
              |||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db        682 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCA 741

Qy        275 AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGA 334
              |||| ||||| |||||||||||||||||||||| |||||||||| || || |||||||
Db        742 AGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGA 801

Qy        335 CCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCC 394
              | || ||||||||||||||||||||| ||||||   |||||||||||||| ||||||||||
Db        802 CGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCC 861

Qy        395 TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
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Db        862 TCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 905


RESULT 4
US-08-318-193-1
; Sequence 1, Application US/08318193
; Patent No. 5641663
;  GENERAL INFORMATION:
;    APPLICANT:  GARVIN, Robert T.
;    APPLICANT:  MALEK, Lawrence T.
;    TITLE OF INVENTION:  AN EXPRESSION SYSTEM FOR THE SECRETION
;    TITLE OF INVENTION:  OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
;    TITLE OF INVENTION:  STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
;    TITLE OF INVENTION:  PROTEINS FROM STREPTOMYCES
;    NUMBER OF SEQUENCES:  91
```

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,193
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,314
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/224,568
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  18740/116 CACO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  392 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA oligonucleotide
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  5..385
US-08-318-193-1

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Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
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Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
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RESULT 5
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;Patent No. 5200327
;    APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
;    TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
;STREPTOMYCES
;    NUMBER OF SEQUENCES: 24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/224,568
;      FILING DATE: 26-JUL-1988
;SEQ ID NO:2:
;      LENGTH: 896
5200327-2

  Query Match             69.5%;  Score 318.4;  DB 6;  Length 896;
  Best Local Similarity   89.3%;  Pred. No. 1.5e-60;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
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Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
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RESULT 6
5200327-2
;Patent No. 5200327
;    APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
;    TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
;STREPTOMYCES
;    NUMBER OF SEQUENCES: 24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/224,568
;      FILING DATE: 26-JUL-1988
;SEQ ID NO:2:
;      LENGTH: 896
5200327-2

  Query Match             69.5%;  Score 318.4;  DB 6;  Length 896;
  Best Local Similarity   89.3%;  Pred. No. 1.5e-60;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
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Db        573 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 632

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||| |||||||||  | |||||||| || ||||||||||||||||||||||
Db        633 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 692

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||||||||||| ||||| |||||||||||||||||||||| ||||| |||||||||
Db        693 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 752

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              |||||||||||||| |||||||||| || || |||||||| || ||||||||||||||||
Db        753 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 812

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| |||||||||||||||||||||| ||||||
Db        813 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 872

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||||||||||||||
Db        873 TGCTGGGAGCCGGTGCAGGAGTGA 896


RESULT 7
US-08-318-193-7
; Sequence 7, Application US/08318193
; Patent No. 5641663
;  GENERAL INFORMATION:
;    APPLICANT:  GARVIN, Robert T.
;    APPLICANT:  MALEK, Lawrence T.
;    TITLE OF INVENTION:  AN EXPRESSION SYSTEM FOR THE SECRETION
;    TITLE OF INVENTION:  OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
;    TITLE OF INVENTION:  STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
;    TITLE OF INVENTION:  PROTEINS FROM STREPTOMYCES
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,193
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,314
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/224,568
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  18740/116 CACO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  900 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA oligonucleotide
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  399..893
US-08-318-193-7

  Query Match            69.5%;  Score 318.4;  DB 1;  Length 900;
  Best Local Similarity  89.3%;  Pred. No. 1.6e-60;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || ||    ||     ||||| |||||||||||||||||||| ||||||||||||
Db        513 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 572

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              ||||||||| | || |||||||||| || ||||| ||||||||||||||||||||||||
Db        573 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 632

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||| |||||||||  | |||||||| || ||||||||||||||||||||||
Db        633 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 692

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||||||||||| ||||| |||||||||||||||||||||| ||||| |||||||||
Db        693 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 752

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              |||||||||||||| |||||||||| || || |||||||| || ||||||||||||||||
Db        753 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 812

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| |||||||||||||||||||||| ||||||
Db        813 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 872

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||||||||||||||
Db        873 TGCTGGGAGCCGGTGCAGGAGTGA 896


RESULT 8
5200327-1
;Patent No. 5200327
;    APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
;    TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
;STREPTOMYCES
;    NUMBER OF SEQUENCES: 24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/224,568
;      FILING DATE: 26-JUL-1988
;SEQ ID NO:1:
;      LENGTH: 386
5200327-1

  Query Match            68.8%;  Score 315;  DB 6;  Length 386;
  Best Local Similarity  91.7%;  Pred. No. 7.5e-60;
  Matches  333;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy         76 CCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAAC 135
              ||||| |||||||||||||||||||| |||||||||||||||||||| | || ||||||
Db         24 CCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAAC 83

Qy        136 CTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTC 195
              ||||| || ||||| ||||||||||||||||||||||||||||||||| |||||||||
Db         84 CTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTC 143

Qy        196 GATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGC 255
              ||  | |||||||| || |||||||||||||||||||||||||||||||||| |||||
Db        144 GACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGG 203

Qy        256 GGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCAC 315
              |||||||||||||||||||||||| ||||| |||||||||||||||||||||| ||||||
```

```
Db        204 GGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCAC 263

Qy        316 TGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAG 375
              ||||| || || |||||||| || |||||||||||||||||| ||||||   ||||||
Db        264 TGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAG 323

Qy        376 GAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              |||||||| ||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        324 GAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAG 383

Qy        436 TGA 438
              |||
Db        384 TGA 386


RESULT 9
5200327-1
;Patent No. 5200327
;    APPLICANT: GARVIN, ROBERT T.;MALEK, LAWRENCE T.
;    TITLE OF INVENTION: EXPRESSION SYSTEM FOR THE SECRETION OF
;BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY STIMULATING
;FACTOR (GM-CSF) AND OTHER HETEROLOGOUS PROTEINS FROM
;STREPTOMYCES
;    NUMBER OF SEQUENCES: 24
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/224,568
;      FILING DATE: 26-JUL-1988
;SEQ ID NO:1:
;      LENGTH: 386
5200327-1

  Query Match             68.8%;  Score 315;  DB 6;  Length 386;
  Best Local Similarity   91.7%;  Pred. No. 7.5e-60;
  Matches  333;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy         76 CCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAAC 135
              ||||| |||||||||||||||||| |||||||||||||||||| | || ||||||
Db         24 CCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAAC 83

Qy        136 CTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTC 195
              ||||| || ||||| |||||||||||||||||||||||||||||||||| |||||||||
Db         84 CTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTC 143

Qy        196 GATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGC 255
              ||  | |||||||| || |||||||||||||||||||||||||||||||||| |||||
Db        144 GACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGG 203

Qy        256 GGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCAC 315
              |||||||||||||||||||||| ||||| |||||||||||||||||||||| ||||||
Db        204 GGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCAC 263

Qy        316 TGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAG 375
              ||||| || || |||||||| || |||||||||||||||||| ||||||   ||||||
Db        264 TGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAG 323

Qy        376 GAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              |||||||| ||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        324 GAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAG 383

Qy        436 TGA 438
              |||
Db        384 TGA 386


RESULT 10
US-10-188-056-31
; Sequence 31, Application US/10188056
; Patent No. 6809191
; GENERAL INFORMATION:
;  APPLICANT: Qiu, Jian-Tai
;  APPLICANT:  Lai, Wan-Ching
;  APPLICANT:  Chu, Yong Liang
;  APPLICANT:  Li, Frank Q.
;  TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
;  FILE REFERENCE: 3781-004-27
;  CURRENT APPLICATION NUMBER: US/10/188,056
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-188-056-31

  Query Match             68.3%;  Score 312.6;  DB 4;  Length 435;
  Best Local Similarity   82.8%;  Pred. No. 2.6e-59;
  Matches  357;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  | ||  |   | |||   |    ||  ||  || || ||  | |
Db          5 GGCTGCAGAGCCTGCTCCTGCTGGGCACCGTGGCCTGCAGCATCAGCGCTCCCGCCAGAA 64

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
              |||| ||||| |||||||||||| |||||||||||||||||| |||||||||||  |||
Db         65 GCCCCAGCCCCTCCACCCAGCCCTGGGAGCACGTGAACGCCATCCAGGAGGCCAGACGGC 124

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              | || ||||| ||| | ||||||||||||||||||||||||||||||||||||||  ||
Db        125 TGCTGAACCTGTCCAGAGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCAGCG 184

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              |||||||||| || |||||||| ||||| || |||||||| || ||||||||||||||||
Db        185 AGATGTTCGACCTGCAGGAGCCCACCTGTCTGCAGACCCGGCTGGAGCTGTACAAGCAGG 244

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              | || || |||||||| |||||||| ||||| || || ||||||||||   ||||||||
Db        245 GACTGCGGGGCAGCCTGACCAAGCTGAAGGGACCCCTGACCATGATGGCCAGCCACTACA 304

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || || || ||||||  |||||||||||||||||||||||||||||
Db        305 AGCAGCACTGCCCTCCCACACCCGAGACCAGCTGCGCCACCCAGATCATCACCTTCGAGA 364

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              |||||||||||||||| |||||||||| || |||||||| |||||||||||||||||| |
Db        365 GCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGACTGCTGGGAGCCCG 424

Qy        428 TGCAGGAGTGA 438
              |||||||||||
Db        425 TGCAGGAGTGA 435


RESULT 11
US-10-188-056-33
; Sequence 33, Application US/10188056
; Patent No. 6809191
; GENERAL INFORMATION:
;  APPLICANT: Qiu, Jian-Tai
;  APPLICANT:  Lai, Wan-Ching
;  APPLICANT:  Chu, Yong Liang
;  APPLICANT:  Li, Frank Q.
;  TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
;  FILE REFERENCE: 3781-004-27
;  CURRENT APPLICATION NUMBER: US/10/188,056
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-188-056-33

  Query Match             67.9%;  Score 311;  DB 4;  Length 435;
  Best Local Similarity   82.6%;  Pred. No. 5.7e-59;
  Matches  356;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;
```

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Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  | ||  |    | |||    |    ||  ||  || || ||  | |
Db          5 GGCTGCAGAGCCTGCTCCTGCTGGGCACCGTGGCCTGCAGCATCAGCGCTCCCGCCAGAA 64

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
              |||| |||| |||||||||| |||||||||||||||| |||||||||||| |   |||
Db         65 GCCCCAGCCCCTCCACCCAGCCCTGGGAGCACGTGAACGCCATCCAGGAGGCCAGACGGC 124

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              | || ||||| ||| | ||||||||||||||||||||||||||||||||||||||   ||
Db        125 TGCTGAACCTGTCCAGAGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCAGCG 184

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              |||||||||| || |||||||| ||||| || |||||||| || ||||||||||||||||
Db        185 AGATGTTCGACCTGCAGGAGCCCACCTGTCTGCAGACCCGGCTGGAGCTGTACAAGCAGG 244

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              | || || |||||||| |||||||| ||||| || || ||||||||||   ||||||||
Db        245 GACTGCGGGGCAGCCTGACCAAGCTGAAGGGACCCCTGACCATGATGGCCAGCCACTACA 304

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || || || ||||||  |||||||||||||| ||||||||||||||
Db        305 AGCAGCACTGCCCTCCCACACCCGAGACCAGCTGCGCCACCCAGACCATCACCTTCGAGA 364

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              |||||||||||||||| |||||||||| || |||||||| ||||||||||||||||| |
Db        365 GCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGACTGCTGGGAGCCCG 424

Qy        428 TGCAGGAGTGA 438
              ||||||||||
Db        425 TGCAGGAGTGA 435
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RESULT 12
US-08-469-318-55
; Sequence 55, Application US/08469318
; Patent No. 6022535
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 196
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/446,872
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-469-318-55

Query Match 61.9%; Score 283.6; DB 3; Length 777;
Best Local Similarity 81.6%; Pred. No. 5.8e-53;
Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

```
Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
              || |||  ||    |  |||||| || || ||   ||||  |||||| ||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
                || |||||||| || ||||||||||||||  | |||||  |||||      | |||||  ||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
              || |||||||| || || || || ||||| || || ||||| || ||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
              ||||| |||||||||||| |||||||||||||||||||||| || ||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
              ||||||||  | ||||||||||   |||||||||||||||||||||| || |||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
              || ||||| || |||||||| |||||||| || || ||||| |||||||| |||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              || || || ||||| || |||||||||||||| || ||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777
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RESULT 13
US-08-468-609A-55
; Sequence 55, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Braford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maire H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olins, Peter O.
; APPLICANT: Paik, Kumnan
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

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;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-468-609A-55

  Query Match             61.9%;  Score 283.6;  DB 3;  Length 777;
  Best Local Similarity   81.6%;  Pred. No. 5.8e-53;
  Matches  328;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
              || ||| ||    | |||||| || || ||   ||||  |||||| ||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
              || |||||||| || ||||||||||||||  | ||||| |||||      | ||||| ||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
              || |||||||| || || || || ||||| || || ||||| || ||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
              ||||| |||||||||||| |||||||||||||||||||| || ||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
              ||||||||  | ||||||||||   |||||||||||||||||||||| || ||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
              || ||||| || |||||||| |||||||| || || ||||| |||||||| |||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              || || || ||||| || |||||||||||||| || ||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777


RESULT 14
US-08-446-872A-55
; Sequence 55, Application US/08446872A
; Patent No. 6361977
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis
;    TITLE OF INVENTION:  Fusion Protein
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,872A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  777 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-446-872A-55

  Query Match             61.9%;  Score 283.6;  DB 3;  Length 777;
  Best Local Similarity   81.6%;  Pred. No. 5.8e-53;
  Matches  328;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
              || ||| ||    | |||||| || || ||   ||||  |||||| ||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
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Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
              || |||||||| || || || || ||||| || || ||||| || ||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
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Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
              ||||||||  | ||||||||||   |||||||||||||||||||||| || ||||||||
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Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              || || || ||||| || |||||||||||||| || ||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777


RESULT 15
US-08-762-227A-55
; Sequence 55, Application US/08762227A
; Patent No. 6436387
;  GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
;                  Caparon, Maire H.
;                  Easton, Alan M.
;                  Klein, Barbara K.
;                  McKearn, John P.
;                  Olins, Peter O.
;                  Paik, Kumnan
;                  Thomas, John W.
;       TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
;                           Fusion Protein
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
;                       Corporate Patent Dept.
;            STREET: P. O. Box 5110
```

```
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60680
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/762,227A
;             FILING DATE: 09-Dec-1996
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bennett, Dennis A.
;             REGISTRATION NUMBER: 34,547
;             REFERENCE/DOCKET NUMBER: C-2790/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (708)470-6501
;             TELEFAX: (708)470-6881
;   INFORMATION FOR SEQ ID NO: 55:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 777 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-08-762-227A-55

  Query Match             61.9%;  Score 283.6;  DB 3;  Length 777;
  Best Local Similarity   81.6%;  Pred. No. 5.8e-53;
  Matches  328;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
              || |||  ||    |  |||||| || || ||   ||||  |||||| ||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
              || |||||||| || |||||||||||||||  | ||||| |||||     | |||||| ||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
              || |||||||| || || || || ||||| || || ||||| || ||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
              |||||| |||||||||||| |||||||||||||||||||| || ||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
              ||||||||  | ||||||||||   |||||||||||||||||||| || ||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
              || ||||| || |||||||| |||||||| || || ||||| |||||||| |||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              || || || ||||| || |||||||||||||| || ||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777


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GenCore version 5.1.6

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Run on: March 11, 2005, 15:19:06 ; Search time 2523 Seconds
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	9	273.6	59.7	592	7	CF370966	CF370966 TgESTzyj5
	10	268.8	58.7	585	7	CF370833	CF370833 TgESTzyj5
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	18	207.2	45.2	672	7	CF614774	CF614774 CES009198
	19	202.4	44.2	511	6	CB430266	CB430266 606148 MA
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	24	175.2	38.3	423	2	AW784714	AW784714 zb77g08.g
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	26	139	30.3	274	1	AA361936	AA361936 EST71529
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	30	104.8	22.9	269	7	CF370885	CF370885 TgESTzyj5
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	37	63.8	13.9	697	9	AG112609	AG112609 Pan trogl
	38	59.8	13.1	457	5	BQ620656	BQ620656 TaLr1135H
	39	59	12.9	160	7	CF341980	CF341980 TgESTzyj5
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c	41	58.2	12.7	830	9	CW010233	CW010233 ZMMBLa001
	42	58	12.7	136	7	CF341168	CF341168 TgESTzyj4
c	43	57.8	12.6	881	9	CG339578	CG339578 OGWMB73TV
	44	57	12.4	747	9	CL959870	CL959870 OsIFCC036
	45	56.8	12.4	671	6	CD926036	CD926036 G750.119N

ALIGNMENTS

RESULT 1
AW207707
LOCUS AW207707 588 bp mRNA linear EST 02-DEC-1999
DEFINITION UI-H-BI2-age-e-09-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724184 3', mRNA sequence.
ACCESSION AW207707
VERSION AW207707.1 GI:6507203
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 588)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=No.
FEATURES Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2724184"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_Sub4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub4 library is a subtracted library derived from the NCI_CGAP_Sub2 library which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Lei2, NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6,

NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 : LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4 pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615) NCI_CGAP_Co10 pool 1 : LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]
TAG_TISSUE=colon
TAG_LIB=NCI_CGAP_Co4
TAG_SEQ=CTTCG"

ORIGIN

Query Match 60.4%; Score 276.8; DB 2; Length 588;
Best Local Similarity 77.5%; Pred. No. 7e-50;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
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Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db        101 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 160

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || || ||||| |
Db        161 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 220

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        221 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 280

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||||| | ||||||||||   ||||||||
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Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
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Db        341 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 400

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
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Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        461 TCCAGGAGTGAG 472
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RESULT 2
BE218982
LOCUS BE218982 660 bp mRNA linear EST 03-JUL-2000
DEFINITION hv47a07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176532 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION BE218982
VERSION BE218982.1 GI:8906300
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 660)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 445.
FEATURES Location/Qualifiers
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/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 60.4%; Score 276.8; DB 2; Length 660;
Best Local Similarity 77.5%; Pred. No. 7e-50;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

```
Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
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Db          9 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 68

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
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Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
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Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
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Db        249 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 308

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        309 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 368

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || |||||||||||||| |
Db        369 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 428

Qy        428 TGCAGGAGTGAG 439
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```
                  | ||||||||||
Db        429 TCCAGGAGTGAG 440


RESULT 3
AI912784
LOCUS       AI912784                 666 bp    mRNA    linear   EST 18-DEC-1999
DEFINITION  we13f07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340997 3'
            similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
            FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI912784
VERSION     AI912784.1  GI:5632639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 743   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 447.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:2340997"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu24"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
                     clones made from the same library (cloneIDs
                     1414920-1417991 and 1520904-1522439). Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match           60.4%;  Score 276.8;  DB 1;  Length 666;
  Best Local Similarity   77.5%;  Pred. No. 7e-50;
  Matches  335;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |     | | |    |    ||  |   || || || |||
Db          9 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 68

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db         69 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 128

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||      | ||||| || || |||||||| || || || || || ||||| |
Db        129 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 188

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||

Db        189 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 248

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||||||  | ||||||||||   ||||||||
Db        249 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 308

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        309 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 368

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || ||||||||||||||| |
Db        369 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 428

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        429 TCCAGGAGTGAG 440


RESULT 4
BE671554
LOCUS       BE671554                 672 bp    mRNA    linear   EST 08-SEP-2000
DEFINITION  7e53h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3286237 3'
            similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
            FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   BE671554
VERSION     BE671554.1  GI:10032095
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 672)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck; M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 440.
FEATURES             Location/Qualifiers
     source          1. .672
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3286237"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu24"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
                     clones made from the same library (cloneIDs
                     1414920-1417991 and 1520904-1522439). Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match           60.4%;  Score 276.8;  DB 2;  Length 672;
  Best Local Similarity   77.5%;  Pred. No. 7e-50;
  Matches  335;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;
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Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |     | | |    |    ||  |   || || || |||
Db         16 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 75

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| |||||| |||||||| ||||| || ||||||||||||||   | |
Db         76 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 135

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || || ||||| |
Db        136 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 195

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        196 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 255

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||| | ||||||||||   ||||||||
Db        256 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 315

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        316 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 375

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || ||||||||||||| |
Db        376 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 435

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        436 TCCAGGAGTGAG 447
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RESULT 5
BE669962
LOCUS BE669962 695 bp mRNA linear EST 08-SEP-2000
DEFINITION 7e27g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3283742 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION BE669962
VERSION BE669962.1 GI:10030503
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 695)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 456.
FEATURES Location/Qualifiers
source 1. .695
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3283742"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Query Match 60.4%; Score 276.8; DB 2; Length 695;
Best Local Similarity 77.5%; Pred. No. 7e-50;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

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Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |     | | |    |    ||  |   || || || |||
Db         45 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 104

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| |||||| |||||||| ||||| || ||||||||||||||   | |
Db        105 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 164

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || || ||||| |
Db        165 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 224

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        225 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 284

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||| | ||||||||||   ||||||||
Db        285 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 344

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        345 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 404

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || |||||||||||||| |
Db        405 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 464

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        465 TCCAGGAGTGAG 476
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RESULT 6
BE873976
LOCUS BE873976 895 bp mRNA linear EST 20-OCT-2000
DEFINITION 601484045F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886571 5', mRNA sequence.
ACCESSION BE873976
VERSION BE873976.1 GI:10322752
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 895)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9663 row: j column: 12

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          High quality sequence stop: 711.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3886571"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
ORIGIN

  Query Match             60.4%;  Score 276.8;  DB 2;  Length 895;
  Best Local Similarity   77.5%;  Pred. No. 7.1e-50;
  Matches  335;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |     | | |    |    ||  |   || || || |||
Db          3 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 62

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
               || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db         63 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 122

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || || ||||| |
Db        123 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 182

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        183 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 242

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||| | ||||||||||   ||||||||
Db        243 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 302

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        303 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 362

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || ||||||||||||||| |
Db        363 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 422

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        423 TCCAGGAGTGAG 434


RESULT 7
BX111836/c
LOCUS       BX111836                658 bp    mRNA    linear   EST 07-FEB-2003
DEFINITION  BX111836 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGp998C104061 ;
            IMAGE:1601601, mRNA sequence.
ACCESSION   BX111836
VERSION     BX111836.1  GI:27837278
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 658)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998C104061.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Heubnerweg 6, D-14059 Berlin, Germany
            Tel: +49 30 32639 101
            Fax: +49 30 32639 111
            www.rzpd.de
            This clone is available royalty-free from RZPD;
            contact RZPD (clone@rzpd.de) for further information. Seq primer:
            M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.
FEATURES             Location/Qualifiers
     source          1. .658
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGp998C104061 ; IMAGE:1601601"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu5"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match             60.3%;  Score 276.2;  DB 5;  Length 658;
  Best Local Similarity   82.3%;  Pred. No. 9.5e-50;
  Matches  317;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || |||   || |||||   ||| ||||| |||||||| ||||| || ||||||
Db        619 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 560

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              ||||||||  | ||||| |||||     | ||||| || || |||||||| || || ||
Db        559 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 500

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              || || ||||| || ||||| || |||||||||||||||||||| |||||||||| |||
Db        499 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 440

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              |||||||||||||||| || |||||||||||||||||||||||  | |||||||||
Db        439 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 380

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              ||  |||||||||||||||||||| || |||||||| || ||||| || ||||||||
Db        379 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 320

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              |||||||| || ||||| |||||||| |||||||| || || || ||||| || |||
Db        319 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 260

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGAG 439
              |||||||||| || ||||||||||
Db        259 TGCTGGGAGCCAGTCCAGGAGTGAG 235


RESULT 8
CF341802
LOCUS       CF341802                584 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  TgESTzyj43f02.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
            cDNA clone TgESTzyj43f02.y1 5' similar to SW:CSF2_HUMAN P04141
            GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
            sequence.
ACCESSION   CF341802
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VERSION     CF341802.1  GI:33831915
KEYWORDS    EST.
SOURCE      Toxoplasma gondii
  ORGANISM  Toxoplasma gondii
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
            Sarcocystidae; Toxoplasma.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
            Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
            Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
            Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
            Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
  TITLE     Toxoplasma EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Clifton, S.
            Toxoplasma EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: toxo@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .584
                     /organism="Toxoplasma gondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:5811"
                     /clone="TgESTzyj43f02.y1"
                     /dev_stage="Tachyzoite"
                     /lab_host="ElectroTen Blue cells (Stratagene)"
                     /clone_lib="Tg CAST Tachyzoite cDNA Library"
                     /note="Vector: Modified pBluescript (pBS SK+); Site_1:
                     BamH1; Site_2: EcoR1; The cDNA library was constructed by
                     Keliang Tang, and Robert Cole at Washington University.
                     cDNA was synthesized from poly(A)+ mRNA using the
                     template-switching PCR method (SMART cDNA Kit, BD
                     Biosciences). First strand cDNA was reverse transcribed
                     using the CDS III/3' primer and a 5' template switch
                     primer (Smart IV primer). The product of the first strand
                     synthesis was PCR amplified using the same primer set and
                     the fragments were digested with SfiI. The fragments were
                     size selected, ligated into a modified pBluescript vector
                     (obtained from Michael White, Montana State University)
                     containing directional SfiI sites, and electroporated into
                     ElectroTen Blue cells. Vector: SfiI sites were added to
                     the multiple cloning region of pBluescript SK+ between the
                     BamHI/EcoRI sites. The modified polylinker has the
                     following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--
                     GGCCGCCTCGGCCCACGGATCC3'where n=3-4 G nucleotides.
                     WARNING: the library contains a small percentage of cDNAs
                     derived from the human host cells. Library materials
                     provided by David Sibley, Washington University."
ORIGIN

  Query Match           60.1%;  Score 275.2;  DB 7;  Length 584;
  Best Local Similarity  77.3%;  Pred. No. 1.6e-49;
  Matches  334;  Conservative    0;  Mismatches   98;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |     | | |    |    ||  |   || || || |||
Db         37 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 96

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                 || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db         97 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 156

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | |||||  || || |||||||| || ||  ||  ||  ||  ||||| |
Db        157 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 216

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | |||||  || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        217 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 276

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              ||||  ||  |||||||||||||||||||||||||||  | ||||||||||   ||||||||
Db        277 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 336

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||||  ||  |||||||  ||  |||||  ||  |||||||  ||||||||  || |
Db        337 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGACTATCACCTTTGAAA 396

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | |||||  ||||||||  ||||||||  ||  ||  ||  |||||  ||  ||||||||||||||  |
Db        397 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 456

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        457 TCCAGGAGTGAG 468


RESULT 9
CF370966
LOCUS       CF370966                592 bp    mRNA    linear   EST 27-AUG-2003
DEFINITION  TgESTzyj58e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
            cDNA clone TgESTzyj58e12.y1 5' similar to SW:CSF2_HUMAN P04141
            GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
            sequence.
ACCESSION   CF370966
VERSION     CF370966.1  GI:34318212
KEYWORDS    EST.
SOURCE      Toxoplasma gondii
  ORGANISM  Toxoplasma gondii
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
            Sarcocystidae; Toxoplasma.
REFERENCE   1  (bases 1 to 592)
  AUTHORS   Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
            Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
            Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
            Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
            Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
  TITLE     Toxoplasma EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Clifton, S.
            Toxoplasma EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: toxo@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .592
                     /organism="Toxoplasma gondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:5811"
                     /clone="TgESTzyj58e12.y1"
                     /dev_stage="Tachyzoite"
                     /lab_host="ElectroTen Blue cells (Stratagene)"
                     /clone_lib="Tg CAST Tachyzoite cDNA Library"
                     /note="Vector: Modified pBluescript (pBS SK+); Site_1:
                     BamH1; Site_2: EcoR1; The cDNA library was constructed by
                     Keliang Tang, and Robert Cole at Washington University.
                     cDNA was synthesized from poly(A)+ mRNA using the
                     template-switching PCR method (SMART cDNA Kit, BD
                     Biosciences). First strand cDNA was reverse transcribed
                     using the CDS III/3' primer and a 5' template switch
                     primer (Smart IV primer). The product of the first strand
                     synthesis was PCR amplified using the same primer set and
                     the fragments were digested with SfiI. The fragments were
                     size selected, ligated into a modified pBluescript vector
                     (obtained from Michael White, Montana State University)
```

containing directional SfiI sites, and electroporated into ElectroTen Blue cells. Vector: SfiI sites were added to the multiple cloning region of pBluescript SK+ between the BamHI/EcoRI sites. The modified polylinker has the following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--GGCCGCCTCGGCCCACGGATCC3'where n=3-4 G nucleotides. WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."

ORIGIN

Query Match 59.7%; Score 273.6; DB 7; Length 592;
Best Local Similarity 77.1%; Pred. No. 3.5e-49;
Matches 333; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

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Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              |||||||   ||  |  | |     | | |     |    ||  |   || || || |||
Db         39 GGATGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 98

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db         99 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 158

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||      | ||||| || || |||||||| || |  || || || ||||| |
Db        159 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGATATAGTAGAAGTCATCTCAG 218

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        219 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 278

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || ||||||| |||||||||||||||||  | ||||||||||   ||||||||
Db        279 GCCTGCGGGGCAGCCCCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 338

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||  |||||||| || |
Db        339 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGACTATCACCTTTGAAA 398

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || |||||||||||||| |
Db        399 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 458

Qy        428 TGCAGGAGTGAG 439
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Db        459 TCCAGGAGTGAG 470
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RESULT 10
CF370833
LOCUS CF370833 585 bp mRNA linear EST 27-AUG-2003
DEFINITION TgESTzyj55e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii cDNA clone TgESTzyj55e12.y1 5' similar to SW:CSF2_HUMAN P04141 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA sequence.
ACCESSION CF370833
VERSION CF370833.1 GI:34318079
KEYWORDS EST.
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.
REFERENCE 1 (bases 1 to 585)
AUTHORS Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
TITLE Toxoplasma EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: toxo@watson.wustl.edu
Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability.
Seq primer: -40UP from Gibco.
FEATURES Location/Qualifiers
source 1. .585
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="TgESTzyj55e12.y1"
/dev_stage="Tachyzoite"
/lab_host="ElectroTen Blue cells (Stratagene)"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/note="Vector: Modified pBluescript (pBS SK+); Site_1: BamH1; Site_2: EcoR1; The cDNA library was constructed by Keliang Tang, and Robert Cole at Washington University. cDNA was synthesized from poly(A)+ mRNA using the template-switching PCR method (SMART cDNA Kit, BD Biosciences). First strand cDNA was reverse transcribed using the CDS III/3' primer and a 5' template switch primer (Smart IV primer). The product of the first strand synthesis was PCR amplified using the same primer set and the fragments were digested with SfiI. The fragments were size selected, ligated into a modified pBluescript vector (obtained from Michael White, Montana State University) containing directional SfiI sites, and electroporated into ElectroTen Blue cells. Vector: SfiI sites were added to the multiple cloning region of pBluescript SK+ between the BamHI/EcoRI sites. The modified polylinker has the following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--GGCCGCCTCGGCCCACGGATCC3'where n=3-4 G nucleotides. WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."

ORIGIN

Query Match 58.7%; Score 268.8; DB 7; Length 585;
Best Local Similarity 76.4%; Pred. No. 3.8e-48;
Matches 330; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

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Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |     | | |     |    ||  |   || || || |||
Db         39 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 98

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db         99 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 158

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||      | ||||| || || |||||||| ||  | || || || ||||| |
Db        159 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATTTAATAGTAGAAGTCATCTCAG 218

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        219 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 278

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || ||||||| |||||||||||||||||  | ||||||||||   ||||||||
Db        279 GCCTGCGGGGCAGCCCCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 338

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||  |||||||| || |
Db        339 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGACTATCACCTTTGAAA 398

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || |||||||||||||| |
Db        399 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 458

Qy        428 TGCAGGAGTGAG 439
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```
Db        459 TCCAGGAGTGAG 470


RESULT 11
CD369973/c
LOCUS       CD369973                718 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT1-bke-o-08-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bke-o-08-0-UI 3', mRNA sequence.
ACCESSION   CD369973
VERSION     CD369973.1  GI:31154063
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 718)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 65-134, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .718
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bke-o-08-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                     moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                     vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                     (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                     3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                     3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                     hours; wt adenovirus + LPS 24 hours. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT1
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

  Query Match           57.8%;  Score 264.8;  DB 6;  Length 718;
  Best Local Similarity  82.3%;  Pred. No. 2.8e-47;
  Matches  316;  Conservative    0;  Mismatches   67;  Indels    1;  Gaps    1;

Qy         56 CGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGG 115
              | || || |||   || |||||   ||| ||||| |||||||| ||||| || |||||||
Db        718 CACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGG 659

Qy        116 AGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGG 175
              ||||||| | ||||| |||||      | ||||| || || |||||||| || || || |
Db        658 AGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAG 599

Qy        176 AGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGC 235
              | || ||||| || ||||| || |||||||||||||||||||| |||||||||| ||||
Db        598 AAGTCATCTCAGAAATGTT-GACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGC 540

Qy        236 TGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGG 295
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Db        539 TGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGG 480

Qy        296 CGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCA 355
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Db        479 CCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTA 420

Qy        356 TCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACT 415
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Db        419 TCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACT 360

Qy        416 GCTGGGAGCCGGTGCAGGAGTGAG 439
              |||||||||| || ||||||||||
Db        359 GCTGGGAGCCAGTCCAGGAGTGAG 336


RESULT 12
BU633411/c
LOCUS       BU633411                701 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FL1-bgu-l-15-0-UI.s1 NCI_CGAP_FL1 Homo sapiens cDNA clone
            UI-H-FL1-bgu-l-15-0-UI 3', mRNA sequence.
ACCESSION   BU633411
VERSION     BU633411.1  GI:23300666
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-46, >AT_rich#Low_complexity 60-129,
            >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .701
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/clone="UI-H-FL1-bgu-1-15-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI_CGAP_FL1"
/note="Organ: Chondrosarcoma; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI_CGAP_FL1 is a normalized cDNA library derived from a pool of mRNA obtained from 4 cell lines from grade III chondrosarcoma tissues. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGGTCGGTG. The cell lines were provided by Dr. James Martin from the University of Iowa.
TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
TAG_LIB=UI-H-FL1
TAG_SEQ=GAGGTCGGTG"

ORIGIN

Query Match 56.5%; Score 258.8; DB 5; Length 701;
Best Local Similarity 83.0%; Pred. No. 5.7e-46;
Matches 307; Conservative 0; Mismatches 62; Indels 1; Gaps 1;

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Qy        70 CCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTC 129
             || |||||   ||| ||||||||||||||| |||||  | ||||||||||||||  | |||
Db       699 CCCAGCCCCAGCACGCAGCCGTGGGAGCATGTGAA-TCCATCCAGGAGGCCCGGCGTCTC 641

Qy       130 CTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAG 189
             || |||||     | ||||| || || |||||||| || || || || || ||||| ||
Db       640 CTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAA 581

Qy       190 ATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGC 249
             ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||||
Db       580 ATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGC 521

Qy       250 CTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACAAG 309
             || || ||||||||||||||||||||||||||  | ||||||||||   ||||||||||
Db       520 CTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACAAG 461

Qy       310 CAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGC 369
             ||||| ||||| || |||||||| || ||||| || |||||||| |||||||| || ||
Db       460 CAGCAGTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGT 401

Qy       370 TTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTG 429
             ||||| |||||||| |||||||| || || || ||||| || ||||||||||||||| ||
Db       400 TTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTC 341

Qy       430 CAGGAGTGAG 439
             ||||||||||
Db       340 CAGGAGTGAG 331
```

RESULT 13
BF938995
LOCUS BF938995 565 bp mRNA linear EST 22-JAN-2001
DEFINITION 7r03f11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3706893 3' similar to SW:CSF2_HUMAN P04141 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA sequence.
ACCESSION BF938995
VERSION BF938995.1 GI:12356315
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 565)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 497.
FEATURES Location/Qualifiers
source 1. .565
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3706893"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 56.0%; Score 256.4; DB 2; Length 565;
Best Local Similarity 77.4%; Pred. No. 1.9e-45;
Matches 336; Conservative 0; Mismatches 96; Indels 2; Gaps 2;

```
Qy         8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
             || ||||   ||  |  | |     | | |    |   ||  |   || || || |||
Db        45 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 104

Qy        68 GCCCGAGCCCGTCCACCCAG-CCGTGGGAGCACGTGAACGCGATC-CAGGAGGCCCGCAG 125
             || |||||   ||| ||| |||||||||||| ||||| || ||| |||||||||||  |
Db       105 CGCCCAGCCCCAGCACGCAGCCCGTGGGAGCATGTGAATGCCATCACAGGAGGCCCGGCG 164

Qy       126 GCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTC 185
             |||||  |||||     | ||||| || || |||||||| || || || || || |||||
Db       165 TCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTC 224

Qy       186 CGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCA 245
             || ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db       225 AGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCA 284

Qy       246 GGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTA 305
             ||||||  || |||||||||||||||||||||||  | ||||||||||   ||||||
Db       285 GGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTA 344

Qy       306 CAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGA 365
             |||||||||||||| || |||||||| || ||||| || |||||||| |||||||| ||
Db       345 CAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGA 404

Qy       366 GAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCC 425
             || ||||| |||||||| |||||||| || || || ||||| || ||||||||||||||
Db       405 AAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCC 464

Qy       426 GGTGCAGGAGTGAG 439
             || ||||||||||
Db       465 AGTCCAGGAGTGAG 478
```

```
RESULT 14
CA307828/c
LOCUS       CA307828                666 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT1-bhx-f-10-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bhx-f-10-0-UI 3', mRNA sequence.
ACCESSION   CA307828
VERSION     CA307828.1  GI:24470882
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-50, >AT_rich#Low_complexity 64-133,
            >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bhx-f-10-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                     moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                     vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                     (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                     3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                     3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                     hours; wt adenovirus + LPS 24 hours. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT1
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

  Query Match           53.2%;  Score 243.6;  DB 6;  Length 666;
  Best Local Similarity  83.4%;  Pred. No. 1.1e-42;
  Matches  276;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy        109 ATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAG 168
              ||||||||||||||  | |||||  |||||      | |||||  ||  || ||||||||  ||
Db        665 ATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAA 606

Qy        169 ACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGC 228
              ||  ||  ||  ||  |||||  ||  |||||  ||  ||||||||||||||||||||  |||||||||
Db        605 ACAGTAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGC 546

Qy        229 CTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACC 288
              |  ||||||||||||||||||||  ||  ||||||||||||||||||||||||||  | |||
Db        545 TTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACC 486

Qy        289 ATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACC 348
              ||||||||   |||  ||||||||||||||||||  ||  ||||||||  ||  |||||  ||  |||
Db        485 ATGATGGCCAGCCANTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACC 426

Qy        349 CAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCG 408
              |||||  ||||||||  ||  ||  |||||  ||||||||  ||||||||  ||  ||  ||  |||||
Db        425 CAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCC 366

Qy        409 TTCGACTGCTGGGAGCCGGTGCAGGAGTGAG 439
              ||  ||||||||||||||  ||  ||||||||||
Db        365 TTTGACTGCTGGGAGCCAGTCCAGGAGTGAG 335


RESULT 15
CD368851/c
LOCUS       CD368851                661 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT1-bjx-m-02-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bjx-m-02-0-UI 3', mRNA sequence.
ACCESSION   CD368851
VERSION     CD368851.1  GI:31152941
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 661)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Distribution information can be found at
            http://genome.uiowa.edu/distribution/cgap.html
             The following repetitive elements were found in this cDNA
            sequence: 65-134, >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .661
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bjx-m-02-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
```

NCI_CGAP_FT1 is a normalized cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500, 3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3 hours; wt adenovirus + LPS 24 hours. The library was normalized according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GGCCATGCCG. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG_TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT1
TAG_SEQ=GGCCATGCCG"

ORIGIN

Query Match 50.4%; Score 230.8; DB 6; Length 661;
Best Local Similarity 83.5%; Pred. No. 6.7e-40;
Matches 273; Conservative 0; Mismatches 53; Indels 1; Gaps 1;

```
Qy        113 AGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCG 172
              ||||||||||  | |||||  |||||      | |||||  ||  ||  ||||||||  ||  ||  |
Db        661 AGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAG 602

Qy        173 TGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCG 232
              | ||  ||  |||||  ||  |||  |  ||  ||||||||||||||||||||  ||||||||||  |
Db        601 TAGAAGTCATCTCAGAAATG-TNGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGG 543

Qy        233 AGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGA 292
              ||||||||||||||||||  ||  ||||||||||||||||||||||||||  |  |||||||
Db        542 AGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGA 483

Qy        293 TGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGA 352
              ||||  ||||||||||||||||||||  ||  ||||||||  ||  |||||  ||  |||||||
Db        482 TGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGA 423

Qy        353 TCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCG 412
              | ||||||||  ||  ||  |||||  ||||||||  ||||||||  ||  ||  |||||  ||  |
Db        422 TTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTG 363

Qy        413 ACTGCTGGGAGCCGGTGCAGGAGTGAG 439
              ||||||||||||  ||  ||||||||||
Db        362 ACTGCTGGGAGCCAGTCCAGGAGTGAG 336
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Search completed: March 11, 2005, 17:24:17
Job time : 2532 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: March 11, 2005, 09:51:36 ; Search time 420 Seconds
(without alignments)
6455.337 Million cell updates/sec

Title: US-10-723-083-1
Perfect score: 458
Sequence: 1 cggcccgggatgcaccacca.....gctagcgtcgacgcatgccg 458

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	319.2	69.7	905	2	AAQ03221	Aaq03221 DNA fragm
2	318.4	69.5	896	2	AAQ03220	Aaq03220 DNA fragm
3	315	68.8	386	2	AAQ03219	Aaq03219 DNA fragm
4	312.6	68.3	435	12	ADI20788	Adi20788 Human GM-
5	311	67.9	435	12	ADI20790	Adi20790 Human GM-
6	284.4	62.1	435	12	ADQ76023	Adq76023 Human GM-
7	283.6	61.9	777	2	AAQ97169	Aaq97169 pMON13022
8	283.6	61.9	777	3	AAA03723	Aaa03723 Human int
9	283.6	61.9	777	6	ABX00012	Abx00012 Human int
10	283.6	61.9	777	12	ADJ14267	Adj14267 DNA relat
11	283	61.8	402	2	AAQ97208	Aaq97208 pMON13012
12	283	61.8	402	3	AAA03771	Aaa03771 Human G-C
13	283	61.8	402	6	ABX00086	Abx00086 Human int
14	283	61.8	402	12	ADJ14388	Adj14388 DNA relat
15	281	61.4	822	2	AAQ97183	Aaq97183 pMON13035
16	281	61.4	822	3	AAA03737	Aaa03737 Human int
17	281	61.4	822	6	ABX00026	Abx00026 Human int
18	281	61.4	822	12	ADJ14281	Adj14281 DNA relat
19	281	61.4	903	2	AAQ97180	Aaq97180 pMON13031
20	281	61.4	903	3	AAA03734	Aaa03734 Human int
21	281	61.4	903	6	ABX00023	Abx00023 Human int
22	281	61.4	903	12	ADJ14278	Adj14278 DNA relat
23	277.8	60.7	1538	10	ADF31962	Adf31962 Human GM-
24	277.8	60.7	1538	10	ADF31989	Adf31989 Human gra
25	277.6	60.6	415	1	AAN90383	Aan90383 Synthetic
26	277.6	60.6	415	1	AAN90274	Aan90274 Synthetic
27	277	60.5	2211	12	ADL16719	Adl16719 Human stu
28	276.8	60.4	448	12	ADL16729	Adl16729 Human gra
29	276.8	60.4	763	2	AAQ04018	Aaq04018 Granulocy
30	276.8	60.4	781	12	ADN07714	Adn07714 Human G-C
31	276.8	60.4	781	12	ADP10387	Adp10387 Reference
32	276.8	60.4	787	1	AAN60364	Aan60364 Human gra
33	276.8	60.4	787	2	AAQ84865	Aaq84865 Clone pcD
34	276.8	60.4	789	3	AAA35017	Aaa35017 Human ade
35	276.8	60.4	789	3	AAF21139	Aaf21139 Human low
36	276.8	60.4	789	4	AAH28217	Aah28217 Nucleotid
37	276.8	60.4	789	10	ABZ96833	Abz96833 Human nuc
38	276.8	60.4	789	11	ABD20682	Abd20682 Human pul
39	276.8	60.4	2385	2	AAT72725	Aat72725 Her2-GM-C
40	276.8	60.4	5115	3	AAA35020	Aaa35020 Human ade
41	276.8	60.4	5115	3	AAF21142	Aaf21142 Human low
42	276.8	60.4	5115	10	ABZ96836	Abz96836 Human nuc
43	276.8	60.4	5115	11	ABD20685	Abd20685 Human pul
44	276.8	60.4	9629	2	AAT14600	Aat14600 pXJCL-hGM
45	276.2	60.3	1011	8	ABX63509	Abx63509 Human cDN

ALIGNMENTS

RESULT 1
AAQ03221
ID AAQ03221 standard; DNA; 905 BP.
XX
AC AAQ03221;
XX
DT 12-JUL-1990 (first entry)
XX
DE DNA fragment of pAEO-GMCSF encodes granulocyte macrophage colony
DE stimulating factor (GM-CSF).
XX
KW Granulocyte macrophage; colony stimulating factor; GM-CSF; cancer; ds.
XX
OS Streptomyces sp.
XX
PN EP352707-A.
XX
PD 31-JAN-1990.
XX
PF 24-JUL-1989; 89EP-00113607.
XX
PR 25-JUL-1988; 88CA-00572956.
XX
PA (CANG-) CANGENE CORP.
XX
PI Garvin RT, Malek LT;
XX
DR WPI; 1990-031296/05.
XX
PT gene expression system directing secretion of protein in Streptomyces -
PT contg. structural gene, esp. for granulocyte macrophage colony
PT stimulating factor, and regulatory sequence.
XX
PS Disclosure; Fig 4; 39pp; English.
XX
CC GM-CSF, or a wide range of other proteins, is secreted in unglycosylated
CC form, with correctly positioned intramolecular disulphide bonds and full
CC biological activity. pAEO.GMCSF contains the BamHI HindIII fragment with
CC an aminoglycoside phosphotransferase promotor and the protease B-endo H
CC hybrid signal peptide. GM-CSF is potentially useful in cancer treatment
XX
SQ Sequence 905 BP; 131 A; 367 C; 298 G; 109 T; 0 U; 0 Other;

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  Query Match             69.7%;  Score 319.2;  DB 2;  Length 905;
  Best Local Similarity   86.9%;  Pred. No. 5.8e-49;
  Matches  351;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         35 CCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGG 94
              ||| |  || ||         || || || ||     ||    ||||| ||||||||||||
Db        502 CCGCCTCCGGGGCGTCTGCAGCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGG 561

Qy         95 AGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCG 154
              ||||||| |||||||||||||||||||| | || |||||||||| || |||||  ||||
Db        562 AGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCG 621

Qy        155 CCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCT 214
              |||||||||||||||||||||||||||||||||| ||||||||||  | ||||||| || |
Db        622 CCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGT 681

Qy        215 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCA 274
              |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db        682 GCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCA 741

Qy        275 AGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGA 334
              ||||  ||||| |||||||||||||||||||||| |||||||||| || || |||||||
Db        742 AGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCACTGCCCCCCCCACGCCGGAGA 801

Qy        335 CCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCC 394
              | || |||||||||||||||||||||||| ||||||   |||||||||||||||||||||
Db        802 CGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCC 861

Qy        395 TCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||| |||||||||||||||||||||||||||||
Db        862 TCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAGTGA 905
```

RESULT 2
AAQ03220
ID AAQ03220 standard; DNA; 896 BP.
XX
AC AAQ03220;
XX
DT 12-JUL-1990 (first entry)
XX
DE DNA fragment of pAPO-GMCSF encodes granulocyte macrophage colony
DE stimulating factor (GM-CSF).
XX
KW Granulocyte macrophage; colony stimulating factor; GM-CSF; cancer; ds.
XX
OS Streptomyces sp.
XX
PN EP352707-A.
XX
PD 31-JAN-1990.
XX
PF 24-JUL-1989; 89EP-00113607.
XX
PR 25-JUL-1988; 88CA-00572956.
XX
PA (CANG-) CANGENE CORP.
XX
PI Garvin RT, Malek LT;
XX
DR WPI; 1990-031296/05.
XX
PT gene expression system directing secretion of protein in Streptomyces -
PT contg. structural gene, esp. for granulocyte macrophage colony
PT stimulating factor, and regulatory sequence.
XX
PS Disclosure; Fig 3; 39pp; English.
XX
CC GM-CSF, or a wide range of other proteins, is secreted in unglycosylated
CC form, with correctly positioned intramolecular disulphide bonds and full
CC biological activity. pAPO.GMCSF contains the BamHI HindIII fragment with
CC an aminoglycoside phosphotransferase promotor and the protease B signal
CC peptide. GM-CSF is potentially useful in cancer treatment
XX
SQ Sequence 896 BP; 135 A; 364 C; 291 G; 106 T; 0 U; 0 Other;

```
  Query Match             69.5%;  Score 318.4;  DB 2;  Length 896;
  Best Local Similarity   89.3%;  Pred. No. 8.1e-49;
  Matches  343;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || ||    ||     ||||| |||||||||||||||||||| ||||||||||||
Db        513 GCCCCCGCCCGGTCGCCCTCGCCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAG 572

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              ||||||||| | || |||||||||| || ||||| |||||||||||||||||||||||||
Db        573 GAGGCCCGCCGCCTGCTCAACCTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTG 632

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||| |||||||||  | |||||||| || ||||||||||||||||||||||
Db        633 GAGGTGATCTCGGAGATGTTCGACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAG 692

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||||||||||| ||||| |||||||||||||||||||||| ||||| |||||||||
Db        693 CTGTACAAGCAGGGGCTCCGGGGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATG 752

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              ||||||||||||| |||||||||| || || |||||||| || ||||||||||||||||
Db        753 GCGTCCCACTACAAACAGCACTGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATC 812

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              ||||| ||||||   |||||||||||||| ||||||||||||||||||||||| ||||||
Db        813 ATCACGTTCGAGTCGTTCAAGGAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGAC 872

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||||||||||||||
Db        873 TGCTGGGAGCCGGTGCAGGAGTGA 896
```

RESULT 3
AAQ03219
ID AAQ03219 standard; DNA; 386 BP.
XX
AC AAQ03219;
XX
DT 12-JUL-1990 (first entry)
XX
DE DNA fragment encodes granulocyte macrophage colony stimulating factor (GM
DE -CSF).
XX
KW Granulocyte macrophage; colony stimulating factor; GM-CSF; cancer; ds.
XX
OS Streptomyces sp.
XX
PN EP352707-A.
XX
PD 31-JAN-1990.
XX
PF 24-JUL-1989; 89EP-00113607.
XX
PR 25-JUL-1988; 88CA-00572956.
XX
PA (CANG-) CANGENE CORP.
XX
PI Garvin RT, Malek LT;
XX
DR WPI; 1990-031296/05.
XX
PT gene expression system directing secretion of protein in Streptomyces -
PT contg. structural gene, esp. for granulocyte macrophage colony
PT stimulating factor, and regulatory sequence.
XX
PS Claim 4; Fig 1; 39pp; English.
XX
CC GM-CSF, or a wide range of other proteins, is secreted in unglycosylated
CC form, with correctly positioned intramolecular disulphide bonds and full

```
CC   biological activity. GM-CSF is potentially useful in cancer treatment
XX
SQ   Sequence 386 BP; 73 A; 141 C; 116 G; 56 T; 0 U; 0 Other;

  Query Match            68.8%;  Score 315;  DB 2;  Length 386;
  Best Local Similarity  91.7%;  Pred. No. 3.4e-48;
  Matches  333;  Conservative    0;  Mismatches   30;  Indels    0;  Gaps    0;

Qy         76 CCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAAC 135
              ||||| ||||||||||||||||||| |||||||||||||||||||| | || ||||||
Db         24 CCGTCGACCCAGCCGTGGGAGCACGTCAACGCGATCCAGGAGGCCCGCCGCCTGCTCAAC 83

Qy        136 CTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTC 195
              ||||| || ||||| |||||||||||||||||||||||||||||||||| |||||||||
Db         84 CTCTCGCGGGACACGGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCGGAGATGTTC 143

Qy        196 GATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGC 255
              ||  | |||||||| || |||||||||||||||||||||||||||||||||| ||||||
Db        144 GACTTGCAGGAGCCCACGTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGGCTCCGG 203

Qy        256 GGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCAC 315
              |||||||||||||||||||||| ||||| |||||||||||||||||||||| ||||||
Db        204 GGCAGCCTCACCAAGCTCAAGGGGCCGCTGACCATGATGGCGTCCCACTACAAACAGCAC 263

Qy        316 TGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAG 375
              ||||| || || |||||||| || |||||||||||||||||||| ||||||    ||||||
Db        264 TGCCCCCCCACGCCGGAGACGTCGTGCGCCACCCAGATCATCACGTTCGAGTCGTTCAAG 323

Qy        376 GAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              |||||||| |||||||||||||||||||||| |||||||||||||||||||||||||||
Db        324 GAGAACCTGAAGGACTTCCTCCTCGTGATCCCCTTCGACTGCTGGGAGCCGGTGCAGGAG 383

Qy        436 TGA 438
              |||
Db        384 TGA 386


RESULT 4
ADI20788
ID   ADI20788 standard; DNA; 435 BP.
XX
AC   ADI20788;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human GM-CSF associated DNA #1.
XX
KW   mammalian granulocyte macrophage-colony stimulating factor; GM-CSF;
KW   Immunostimulant; Cytostatic; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004004742-A1.
XX
PD   15-JAN-2004.
XX
PF   03-JUL-2003; 2003WO-US020908.
XX
PR   03-JUL-2002; 2002US-00188056.
XX
PA   (VAXI-) VAXIM INC.
XX
PI   Qiu J,  Lai W,  Chu YL,  Li FQ;
XX
DR   WPI; 2004-099342/10.
XX
PT   New DNA sequence comprising a codon optimized sequence encoding a
PT   mammalian granulocyte macrophage-colony stimulating factor, useful as an
PT   adjuvant for enhancing an immune response of a mammal to preventive or
PT   therapeutic vaccine.
XX
PS   Disclosure; SEQ ID NO 31; 42pp; English.
XX
CC   The present invention relates to a DNA sequence comprising a codon-
CC   optimized sequence encoding a mammalian granulocyte macrophage-colony
CC   stimulating factor (GM-CSF), is new, where the codon optimized sequence
CC   is different from the corresponding wild type GM-CSF encoding DNA, where
CC   a codon in the codon optimized sequence has been altered to enhance the
CC   expression of the mammalian GM-CSF. The method is useful as an adjuvant
CC   in gene therapy or in vaccination for enhancing an immune response of a
CC   mammal to a preventive or therapeutic vaccine, is also useful for
CC   treating cancer or for effecting gene therapy. Use of the DNA sequence
CC   comprising a codon optimized sequence encoding a mammalian granulocyte
CC   macrophage-colony stimulating factor as an adjuvant results in improved
CC   adjuvant activity when expressed in vivo compared with the native GM-CSF
CC   gene sequence. The present sequence represents human GM-CSF associated
CC   encoding sequence.
XX
SQ   Sequence 435 BP; 94 A; 151 C; 128 G; 62 T; 0 U; 0 Other;

  Query Match            68.3%;  Score 312.6;  DB 12;  Length 435;
  Best Local Similarity  82.8%;  Pred. No. 9.3e-48;
  Matches  357;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  | ||  |    | |||    |    ||  ||  || || ||  | |
Db          5 GGCTGCAGAGCCTGCTCCTGCTGGGCACCGTGGCCTGCAGCATCAGCGCTCCCGCCAGAA 64

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
              |||| ||||| |||||||||||| |||||||||||||||||| |||||||||||| |  |||
Db         65 GCCCCAGCCCCTCCACCCAGCCCTGGGAGCACGTGAACGCCATCCAGGAGGCCAGACGGC 124

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              | || ||||| ||| | ||||||||||||||||||||||||||||||||||||||  ||
Db        125 TGCTGAACCTGTCCAGAGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCAGCG 184

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              |||||||||| || |||||||| ||||| || |||||||| || ||||||||||||||||
Db        185 AGATGTTCGACCTGCAGGAGCCCACCTGTCTGCAGACCCGGCTGGAGCTGTACAAGCAGG 244

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              | || || |||||||| |||||||| ||||| || || ||||||||||   ||||||||
Db        245 GACTGCGGGGCAGCCTGACCAAGCTGAAGGGACCCCTGACCATGATGGCCAGCCACTACA 304

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||||| || || || ||||||  ||||||||||||||||||||||||||||
Db        305 AGCAGCACTGCCCTCCCACACCCGAGACCAGCTGCGCCACCCAGATCATCACCTTCGAGA 364

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              |||||||||||||||| |||||||||| || |||||||| |||||||||||||||||| |
Db        365 GCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGACTGCTGGGAGCCCG 424

Qy        428 TGCAGGAGTGA 438
              ||||||||||||
Db        425 TGCAGGAGTGA 435


RESULT 5
ADI20790
ID   ADI20790 standard; DNA; 435 BP.
XX
AC   ADI20790;
XX
DT   22-APR-2004  (first entry)
XX
DE   Human GM-CSF associated DNA #3.
XX
KW   mammalian granulocyte macrophage-colony stimulating factor; GM-CSF;
KW   Immunostimulant; Cytostatic; vaccine; ds.
XX
OS   Homo sapiens.
XX
PN   WO2004004742-A1.
XX
PD   15-JAN-2004.
XX
```

PF 03-JUL-2003; 2003WO-US020908.
XX
PR 03-JUL-2002; 2002US-00188056.
XX
PA (VAXI-) VAXIM INC.
XX
PI Qiu J, Lai W, Chu YL, Li FQ;
XX
DR WPI; 2004-099342/10.
XX
PT New DNA sequence comprising a codon optimized sequence encoding a
PT mammalian granulocyte macrophage-colony stimulating factor, useful as an
PT adjuvant for enhancing an immune response of a mammal to preventive or
PT therapeutic vaccine.
XX
PS Disclosure; SEQ ID NO 33; 42pp; English.
XX
CC The present invention relates to a DNA sequence comprising a codon-
CC optimized sequence encoding a mammalian granulocyte macrophage-colony
CC stimulating factor (GM-CSF), is new, where the codon optimized sequence
CC is different from the corresponding wild type GM-CSF encoding DNA, where
CC a codon in the codon optimized sequence has been altered to enhance the
CC expression of the mammalian GM-CSF. The method is useful as an adjuvant
CC in gene therapy or in vaccination for enhancing an immune response of a
CC mammal to a preventive or therapeutic vaccine, is also useful for
CC treating cancer or for effecting gene therapy. Use of the DNA sequence
CC comprising a codon optimized sequence encoding a mammalian granulocyte
CC macrophage-colony stimulating factor as an adjuvant results in improved
CC adjuvant activity when expressed in vivo compared with the native GM-CSF
CC gene sequence. The present sequence represents human GM-CSF associated
CC encoding sequence.
XX
SQ Sequence 435 BP; 94 A; 152 C; 128 G; 61 T; 0 U; 0 Other;

Query Match 67.9%; Score 311; DB 12; Length 435;
Best Local Similarity 82.6%; Pred. No. 1.8e-47;
Matches 356; Conservative 0; Mismatches 75; Indels 0; Gaps 0;

```
Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  | ||  |    | |||    |    ||  ||  || || ||  | |
Db          5 GGCTGCAGAGCCTGCTCCTGCTGGGCACCGTGGCCTGCAGCATCAGCGCTCCCGCCAGAA 64

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
              |||| ||||| |||||||||| |||||||||||||||| |||||||||||  |  |||
Db         65 GCCCCAGCCCCTCCACCCAGCCCTGGGAGCACGTGAACGCCATCCAGGAGGCCAGACGGC 124

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              . | || ||||| ||| | ||||||||||||||||||||||||||||||||||||  ||
Db        125 TGCTGAACCTGTCCAGAGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCAGCG 184

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              |||||||||| || |||||||| ||||| || |||||||| || ||||||||||||||||
Db        185 AGATGTTCGACCTGCAGGAGCCCACCTGTCTGCAGACCCGGCTGGAGCTGTACAAGCAGG 244

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              | || || |||||||| |||||||| ||||| || || ||||||||||   ||||||||
Db        245 GACTGCGGGGCAGCCTGACCAAGCTGAAGGGACCCCTGACCATGATGGCCAGCCACTACA 304

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||||| || || || ||||||  |||||||||||||| ||||||||||||||
Db        305 AGCAGCACTGCCCTCCCACACCCGAGACCAGCTGCGCCACCCAGACCATCACCTTCGAGA 364

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              |||||||||||||| |||||||||| || |||||||| ||||||||||||||||||| |
Db        365 GCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGACTGCTGGGAGCCCG 424

Qy        428 TGCAGGAGTGA 438
              ||||||||||
Db        425 TGCAGGAGTGA 435
```

RESULT 6
ADQ76023

ID ADQ76023 standard; DNA; 435 BP.
XX
AC ADQ76023;
XX
DT 07-OCT-2004 (first entry)
XX
DE Human GM-CSF codon optimised coding sequence.
XX
KW ds; gene; human; GM-CSF; codon optimisation; protein production.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO2004059556-A2.
XX
PD 15-JUL-2004.
XX
PF 23-DEC-2003; 2003WO-EP014850.
XX
PR 23-DEC-2002; 2002DE-01060805.
XX
PA (GENE-) GENEART GMBH.
XX
PI Raab D, Graf M, Notka F, Wagner R;
XX
DR WPI; 2004-543639/52.
XX
PT Computer optimization of a nucleotide sequence for a protein comprises
PT evaluating test sequences with a quality function to determine the
PT optimum sequence.
XX
PS Claim 25; SEQ ID NO 2; 83pp; German.
XX
CC The present invention relates to a method of optimising a coding sequence
CC for expression of a protein, based on the amino acid sequence of the
CC protein. This involves the use of a computer to generate a test sequence
CC with m optimisation positions determined for a defined region, in which
CC positions the codon usage is varied. The optimum codon usage at such
CC positions is determined by means of a power function. The steps are
CC reiterated with different regions of the sequence, with the optimised
CC codons previously identified being left unchanged during subsequent
CC steps. The method can be used for expression of proteins. The present
CC sequence is a codon optimised version of the human GM-CSF coding
CC sequence.
XX
SQ Sequence 435 BP; 101 A; 132 C; 128 G; 74 T; 0 U; 0 Other;

Query Match 62.1%; Score 284.4; DB 12; Length 435;
Best Local Similarity 84.0%; Pred. No. 1.2e-42;
Matches 321; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```
Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || ||  | ||||| |||||   ||| ||||| ||||||||||||| || ||||||
Db         52 GCCCCTGCCAGAAGCCCTAGCCCTAGCACACAGCCTTGGGAGCACGTGAATGCCATCCAG 111

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTG 174
              |||||| | || || || |||||   | | || || |||||||||||||||||||||||
Db        112 GAGGCCAGGAGACTGCTGAACCTGAGCAGAGATACAGCCGCCGAGATGAACGAGACCGTG 171

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              |||||||||  |||||||||||| || |||||||| || ||||| |||||||| || |||
Db        172 GAGGTGATCAGCGAGATGTTCGACCTGCAGGAGCCTACATGCCTGCAGACCCGGCTGGAG 231

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              ||||| ||||||||||  | |||   || |||||||| |||||||| || || ||||||
Db        232 CTGTATAAGCAGGGCCTGAGAGGCTCTCTGACCAAGCTGAAGGGCCCCCTGACAATGATG 291

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              ||   |||||||||||||||||||| || ||||| |||||   ||||||||||||||||
Db        292 GCCAGCCACTACAAGCAGCACTGCCCTCCTACCCCTGAGACAAGCTGCGCCACCCAGATC 351

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              |||||||||||||||||||||||||||||| |||||||||| || |||||||| |||||
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Db        352 ATCACCTTCGAGAGCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGAT 411

Qy        415 TGCTGGGAGCCGGTGCAGGAGT 436
              ||||||||||| ||||||||||
Db        412 TGCTGGGAGCCCGTGCAGGAGT 433


RESULT 7
AAQ97169
ID   AAQ97169 standard; DNA; 777 BP.
XX
AC   AAQ97169;
XX
DT   25-AUG-1999  (first entry)
XX
DE   pMON13022 DNA encoding IL-3 fusion protein.
XX
KW   Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW   mutant; mutein; fusion protein; linker; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9521254-A1.
XX
PD   10-AUG-1995.
XX
PF   02-FEB-1995;   95WO-US001185.
XX
PR   04-FEB-1994;   94US-00192325.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer CS,  Abrams MA,  Braford-Goldberg SR,  Caparon MH,  Easton AM;
PI   Klein BK,  Mckearn JP,  Olins PO,  Paik K,  Thomas JW;
XX
DR   WPI; 1995-283774/37.
DR   P-PSDB; AAR79317.
XX
PT   Fusion proteins comprising a human interleukin-3 variant, a linker and
PT   interleukin-3, a variant or a colony stimulating factor - useful to
PT   increase haematopoietic cell prodn. in a mammal.
XX
PS   Claim 22; Page 158-159; 447pp; English.
XX
CC   A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC   R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC   interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC   including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC   or IL-3 variant, and L is a linker. Generic sequences are described in
CC   AAW03235 - AAW03242, and specifically claimed examples are shown in
CC   AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC   recombinant DNA techniques. Specifically claimed examples of DNA
CC   sequences (including the present sequence) which encode these proteins
CC   are shown in AAQ97167-Q97204 and AAQ97222-Q97227. The fusion protein is
CC   used to increase haematopoietic cell production. It is also useful as an
CC   IL-3 antagonist or as a discrete antigenic fragment for production of
CC   antibodies useful in immunoassays and immunotherapy. Antagonists are used
CC   to block the growth of certain cancer cells and in treatment of asthma.
CC   The fusion protein can also be used to stimulate bone marrow and blood
CC   cell activation and growth in vitro before infusion; and to treat
CC   diseases characterised by decreased levels of myeloid, erythroid,
CC   lymphoid and/or megakaryocyte cells of the haematopoietic system. The
CC   protein has the usual activity of both its component proteins, but may
CC   have increased synergistic activity and reduced undesired side effects
XX
SQ   Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

  Query Match             61.9%;  Score 283.6;  DB 2;  Length 777;
  Best Local Similarity   81.6%;  Pred. No. 1.6e-42;
  Matches  328;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
              || ||| ||    | |||||| || || ||   ||||  |||||| ||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
              || |||||||| || |||||||||||||  | |||||  |||||      | |||||  ||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
              || |||||||| || || || || ||||| || || ||||| || ||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
              ||||| |||||||||||| |||||||||||||||||||| || ||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
              |||||||  | ||||||||||   |||||||||||||||||||| || ||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
              || ||||| || |||||||| |||||||| || || ||||| |||||||| |||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              || || || ||||| || ||||||||||||||| || ||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777


RESULT 8
AAA03723
ID   AAA03723 standard; DNA; 777 BP.
XX
AC   AAA03723;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human interleukin-3 mutant containing fusion protein DNA SEQ ID NO:55.
XX
KW   Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
KW   colony stimulating factor; haematopoietic growth factor; lymphokine;
KW   fusion protein; haematopoietic disorder; infection; cancer;
KW   radiation therapy; chemotherapy; bone marrow suppressive drug;
KW   bone marrow activation; blood cell activation; blood transplant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6022535-A.
XX
PD   08-FEB-2000.
XX
PF   06-JUN-1995;   95US-00469318.
XX
PR   04-FEB-1994;   94US-00192325.
PR   02-FEB-1995;   95WO-US001185.
PR   06-APR-1995;   95US-00411795.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer SC,  Abrams MA,  Braford-Goldberg SR,  Easton AM,  Klein BK;
PI   Paik K,  Thomas JW,  Mckearn JP,  Olins PO,  Caparon MH;
XX
DR   WPI; 2000-160368/14.
XX
PT   Treating hematopoietic disorders with fusion proteins comprising mutated
PT   interleukin-3 fused with secondary colony stimulating factors or other
PT   interleukin-3 variants.
XX
PS   Example 27; Col 135-136; 276pp; English.
XX
CC   Methods have been developed for treating haematopoietic disorders with
CC   fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-
CC   3) variants or mutant proteins (muteins) fused with secondary colony
```

CC stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
CC and/or haematopoietic colony stimulating factors) or other interleukin-3
CC variants with or without a linker. The methods may be used in vivo to
CC treat haematopoietic disorders resulting from bacterial, viral and fungal
CC infections, cancer radiation therapy, chemotherapy or bone marrow
CC suppressive drugs. They may also be used in vitro to stimulate bone
CC marrow and blood cell activation and growth prior to infusion of the bone
CC marrow and blood transplants into patients. IL-3 is a haematopoietic
CC growth factor which has the property of being able to promote the
CC survival, growth and differentiation of haematopoietic cells. The fusion
CC molecules are characterised by possessing the usual activity of both of
CC their constituent peptides and further by having a biological or
CC physiological activity greater than the additive function of the IL-3 or
CC second CSF alone (i.e. the peptides act synergistically). Their activity
CC may also be further enhanced by the mutations they comprise. The
CC variations may further reduce undesirable side effects associated with IL
CC -3. AAY53130 to AAY53226, and AAA03721 to AAA03782 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Query Match 61.9%; Score 283.6; DB 3; Length 777;
Best Local Similarity 81.6%; Pred. No. 1.6e-42;
Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
Db 376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy 94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
Db 436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy 154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
Db 496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy 214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
Db 556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy 274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
Db 616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy 334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
Db 676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy 394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
Db 736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 9
ABX00012
ID ABX00012 standard; DNA; 777 BP.
XX
AC ABX00012;
XX
DT 18-DEC-2002 (first entry)
XX
DE Human interleukin-3 associated DNA sequence #3.
XX
KW Haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; ds;
KW G-CSF; G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
KW human growth hormone; B-cell growth factor; leukaemia;
KW B-cell differentiation factor; eosinophil differentiation factor;
KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
KW myelofibrosis; Interleukin-3; IL-3; stem cell.
XX
OS Unidentified.
XX
PN US6436387-B1.
XX
PD 20-AUG-2002.
XX
PF 09-DEC-1996; 96US-00762227.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 04-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2002-749206/81.
XX
PT Ex vivo expansion of stem cells, for enhancing transduction efficiency of
PT cultured stem cells, comprises culturing stem cells in growth medium
PT having mutant interleukin-3, and hematopoietic factor, and harvesting
PT cultured cells.
XX
PS Disclosure; Col 161-164; 203pp; English.
XX
CC The invention relates to ex vivo expansion of stem cells, comprises
CC culturing stem cells with a growth medium comprising a chimaera protein,
CC and harvesting the cultured stem cells. The chimaera is based on a
CC mutated human interleukin-3 (IL_3) sequence coupled to a haematopoietic
CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
CC CSFSer17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
CC differentiation factor, eosinophil differentiation factor and stem cell
CC factor (SCF)) via a peptide linker. The formula for the chimaera is given
CC in the specification. Also included is a method for enhancing the
CC efficiency of the transduction of cultured stem cells by a heterologous
CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
CC culturing the stem cells with a growth medium comprising the chimaera (c)
CC transducing DNA into cultured cells; and (d) harvesting the transduced
CC cells. The method is useful for ex vivo expansion of stem cells, and
CC enhancing the efficiency of the transduction of cultured stem cells by a
CC heterologous gene. The method is also useful for treating a patient
CC having a haematopoietic disorder. The expanded haematopoietic cells are
CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
CC and myelofibrosis. The present sequence is an IL-3 mutant associated DNA
CC sequence. Note: The present sequence is included in the sequence listing
CC but is not mentioned anywhere else in the specification
XX
SQ Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Query Match 61.9%; Score 283.6; DB 6; Length 777;
Best Local Similarity 81.6%; Pred. No. 1.6e-42;
Matches 328; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
Db 376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy 94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
Db 436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy 154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
Db 496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy 214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273

```
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333

Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393

Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435

Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777
```

RESULT 10
ADJ14267
ID ADJ14267 standard; DNA; 777 BP.
XX
AC ADJ14267;
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID 55.
XX
KW stem cell; antianaemic; immunostimulant; immunomodulator;
KW antiinflammatory; dermatological; immunosuppressive; cytostatic;
KW neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;
KW lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
KW Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
KW myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.
XX
OS Unidentified.
XX
PN US2003185790-A1.
XX
PD 02-OCT-2003.
XX
PF 26-FEB-2002; 2002US-00083446.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 02-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
PR 09-DEC-1996; 96US-00762227.
XX
PA (BAUE/) BAUER S C.
PA (ABRA/) ABRAMS M A.
PA (BRAF/) BRAFORD-GOLDBERG S R.
PA (CAPA/) CAPARON M H.
PA (EAST/) EASTON A M.
PA (KLEI/) KLEIN B K.
PA (MCKE/) MCKEARN J P.
PA (OLIN/) OLINS P O.
PA (PAIK/) PAIK K.
PA (THOM/) THOMAS J W.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2004-096775/10.
XX
PT Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating
PT aplastic anemia, involves culturing the stem cells with growth medium
PT comprising chimera protein, and harvesting the cultured stem cells.
XX
PS Disclosure; SEQ ID NO 55; 202pp; English.
XX
CC The invention relates to a novel method whereby stem cells are ex vivo
CC expanded via culturing the stem cells with a growth medium comprising a
CC chimera protein, followed by harvesting of the cultured stem cells. The
CC method of the invention has antianaemic, immunostimulant,
CC immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC cytostatic and neuroprotective applications and may be useful to target
CC haemopoietic cells for gene therapy, preferably for treating patients
CC having a haemopoietic disorder characterised by decreased levels of
CC myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC system. The expanded ex vivo cells may be used to treat neutropenia,
CC aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC myelofibrosis. The current sequence is that of a DNA related to the human
CC interleukin-3 (IL-3) mutant protein of the invention.
XX
SQ Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

```
  Query Match             61.9%;  Score 283.6;  DB 12;  Length 777;
  Best Local Similarity   81.6%;  Pred. No. 1.6e-42;
  Matches  328;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93

Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153

Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213

Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273

Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333

Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393

Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435

Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777
```

RESULT 11
AAQ97208
ID AAQ97208 standard; DNA; 402 BP.
XX
AC AAQ97208;
XX
DT 25-AUG-1999 (first entry)
XX
DE pMON13012 DNA sequence.
XX
KW Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW mutant; mutein; fusion protein; linker; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9521254-A1.
XX
PD 10-AUG-1995.
XX
PF 02-FEB-1995; 95WO-US001185.
XX
PR 04-FEB-1994; 94US-00192325.
XX
PA (SEAR) SEARLE & CO G D.

```
XX
PI   Bauer CS,  Abrams MA,  Braford-Goldberg SR,  Caparon MH,  Easton AM;
PI   Klein BK,  Mckearn JP,  Olins PO,  Paik K,  Thomas JW;
XX
DR   WPI; 1995-283774/37.
DR   P-PSDB; AAR79338.
XX
PT   Fusion proteins comprising a human interleukin-3 variant, a linker and
PT   interleukin-3, a variant or a colony stimulating factor - useful to
PT   increase haematopoietic cell prodn. in a mammal.
XX
PS   Example 19; Page 183; 447pp; English.
XX
CC   A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC   R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC   interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC   including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC   or IL-3 variant, and L is a linker. Generic sequences are described in
CC   AAW03235 - AAW03242, and specifically claimed examples are shown in
CC   AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC   recombinant DNA techniques. Specifically claimed examples of DNA
CC   sequences which encode these proteins are shown in AAQ97167-Q97204 and
CC   AAQ97222-Q97227. The fusion protein is used to increase haematopoietic
CC   cell production. It is also useful as an IL-3 antagonist or as a discrete
CC   antigenic fragment for production of antibodies useful in immunoassays
CC   and immunotherapy. Antagonists are used to block the growth of certain
CC   cancer cells and in treatment of asthma. The fusion protein can also be
CC   used to stimulate bone marrow and blood cell activation and growth in
CC   vitro before infusion; and to treat diseases characterised by decreased
CC   levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the
CC   haematopoietic system. The protein has the usual activity of both its
CC   component proteins, but may have increased synergistic activity and
CC   reduced undesired side effects
XX
SQ   Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

  Query Match            61.8%;  Score 283;  DB 2;  Length 402;
  Best Local Similarity   83.2%;  Pred. No. 2.1e-42;
  Matches  322;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          52 ATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATC 111
               ||||| || || ||   ||||  |||||| ||||||||||||||| |||||||| || |||
Db           1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         112 CAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACC 171
               ||||||||||  | ||||| |||||     | ||||| || || |||||||| || ||
Db          61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         172 GTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTC 231
               || || ||||| || || ||||| || |||||||||||||| ||||| ||||||||||
Db         121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         232 GAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATG 291
               |||||||||||||||||||| || |||||||||||||||||||||||||  | ||||||
Db         181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         292 ATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAG 351
               |||||   |||||||||||||||||||| || |||||||| || ||||| || ||||||
Db         241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy         352 ATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTC 411
               || |||||||| || || ||||| |||||||| |||||||||| || || ||||| ||
Db         301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy         412 GACTGCTGGGAGCCGGTGCAGGAGTGA 438
               |||||||||||||| || |||||||||
Db         361 GACTGCTGGGAGCCAGTCCAGGAGTGA 387


RESULT 12
AAA03771
ID   AAA03771 standard; DNA; 402 BP.
XX
AC   AAA03771;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human G-CSF mutant DNA sequence SEQ ID NO:176.
XX
KW   Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
KW   colony stimulating factor; haematopoietic growth factor; lymphokine;
KW   fusion protein; haematopoietic disorder; infection; cancer;
KW   radiation therapy; chemotherapy; bone marrow suppressive drug;
KW   bone marrow activation; blood cell activation; blood transplant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6022535-A.
XX
PD   08-FEB-2000.
XX
PF   06-JUN-1995;   95US-00469318.
XX
PR   04-FEB-1994;   94US-00192325.
PR   02-FEB-1995;   95WO-US001185.
PR   06-APR-1995;   95US-00411795.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer SC,  Abrams MA,  Braford-Goldberg SR,  Easton AM,  Klein BK;
PI   Paik K,  Thomas JW,  Mckearn JP,  Olins PO,  Caparon MH;
XX
DR   WPI; 2000-160368/14.
XX
PT   Treating hematopoietic disorders with fusion proteins comprising mutated
PT   interleukin-3 fused with secondary colony stimulating factors or other
PT   interleukin-3 variants.
XX
PS   Example 19; Col 171-174; 276pp; English.
XX
CC   Methods have been developed for treating haematopoietic disorders with
CC   fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-
CC   3) variants or mutant proteins (muteins) fused with secondary colony
CC   stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
CC   and/or haematopoietic colony stimulating factors) or other interleukin-3
CC   variants with or without a linker. The methods may be used in vivo to
CC   treat haematopoietic disorders resulting from bacterial, viral and fungal
CC   infections, cancer radiation therapy, chemotherapy or bone marrow
CC   suppressive drugs. They may also be used in vitro to stimulate bone
CC   marrow and blood cell activation and growth prior to infusion of the bone
CC   marrow and blood transplants into patients. IL-3 is a haematopoietic
CC   growth factor which has the property of being able to promote the
CC   survival, growth and differentiation of haematopoietic cells. The fusion
CC   molecules are characterised by possessing the usual activity of both of
CC   their constituent peptides and further by having a biological or
CC   physiological activity greater than the additive function of the IL-3 or
CC   second CSF alone (i.e. the peptides act synergistically). Their activity
CC   may also be further enhanced by the mutations they comprise. The
CC   variations may further reduce undesirable side effects associated with IL
CC   -3. AAY53130 to AAY53226, and AAA03721 to AAA03782 represent sequences
CC   used in the exemplification of the present invention
XX
SQ   Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

  Query Match            61.8%;  Score 283;  DB 3;  Length 402;
  Best Local Similarity   83.2%;  Pred. No. 2.1e-42;
  Matches  322;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          52 ATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATC 111
               ||||| || || ||   ||||  |||||| ||||||||||||||| |||||||| || |||
Db           1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         112 CAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACC 171
               ||||||||||  | ||||| |||||     | ||||| || || |||||||| || ||
Db          61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120
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Qy        172 GTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTC 231
              || || ||||| || || ||||| || ||||||||||||||| ||||| ||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy        232 GAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATG 291
              |||||||||||||||||||| || ||||||||||||||||||||||||   | ||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy        292 ATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAG 351
              |||||   |||||||||||||||||||| || |||||||| || ||||| || ||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        352 ATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTC 411
              || |||||||| || || ||||| |||||||| |||||||||| || || ||||| ||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        412 GACTGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||| || |||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAGTGA 387
```

RESULT 13
ABX00086
ID ABX00086 standard; DNA; 402 BP.
XX
AC ABX00086;
XX
DT 18-DEC-2002 (first entry)
XX
DE Human interleukin-3 associated DNA sequence #77.
XX
KW Haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; ds;
KW G-CSF; G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
KW human growth hormone; B-cell growth factor; leukaemia;
KW B-cell differentiation factor; eosinophil differentiation factor;
KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
KW myelofibrosis; Interleukin-3; IL-3; stem cell.
XX
OS Unidentified.
XX
PN US6436387-B1.
XX
PD 20-AUG-2002.
XX
PF 09-DEC-1996; 96US-00762227.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 04-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2002-749206/81.
XX
PT Ex vivo expansion of stem cells, for enhancing transduction efficiency of
PT cultured stem cells, comprises culturing stem cells in growth medium
PT having mutant interleukin-3, and hematopoietic factor, and harvesting
PT cultured cells.
XX
PS Disclosure; Col 299-300; 203pp; English.
XX
CC The invention relates to ex vivo expansion of stem cells, comprises
CC culturing stem cells with a growth medium comprising a chimaera protein,
CC and harvesting the cultured stem cells. The chimaera is based on a
CC mutated human interleukin-3 (IL_3) sequence coupled to a haematopoietic
CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
CC CSFSer17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
CC differentiation factor, eosinophil differentiation factor and stem cell
CC factor (SCF)) via a peptide linker. The formula for the chimaera is given
CC in the specification. Also included is a method for enhancing the
CC efficiency of the transduction of cultured stem cells by a heterologous
CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
CC culturing the stem cells with a growth medium comprising the chimaera (c)
CC transducing DNA into cultured cells; and (d) harvesting the transduced
CC cells. The method is useful for ex vivo expansion of stem cells, and
CC enhancing the efficiency of the transduction of cultured stem cells by a
CC heterologous gene. The method is also useful for treating a patient
CC having a haematopoietic disorder. The expanded haematopoietic cells are
CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
CC and myelofibrosis. The present sequence is an IL-3 mutant associated DNA
CC sequence. Note: The present sequence is included in the sequence listing
CC but is not mentioned anywhere else in the specification
XX
SQ Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

  Query Match   61.8%; Score 283; DB 6; Length 402;
  Best Local Similarity 83.2%; Pred. No. 2.1e-42;
  Matches 322; Conservative   0; Mismatches   65; Indels   0; Gaps   0;

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Qy        112 CAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACC 171
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Qy        172 GTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTC 231
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Db        361 GACTGCTGGGAGCCAGTCCAGGAGTGA 387
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RESULT 14
ADJ14388
ID ADJ14388 standard; DNA; 402 BP.
XX
AC ADJ14388;
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID 151.
XX
KW stem cell; antianaemic; immunostimulant; immunomodulator;
KW antiinflammatory; dermatological; immunosuppressive; cytostatic;
KW neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;
KW lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
KW Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
KW myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.

XX
OS Unidentified.
XX
PN US2003185790-A1.
XX
PD 02-OCT-2003.
XX
PF 26-FEB-2002; 2002US-00083446.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 02-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
PR 09-DEC-1996; 96US-00762227.
XX
PA (BAUE/) BAUER S C.
PA (ABRA/) ABRAMS M A.
PA (BRAF/) BRAFORD-GOLDBERG S R.
PA (CAPA/) CAPARON M H.
PA (EAST/) EASTON A M.
PA (KLEI/) KLEIN B K.
PA (MCKE/) MCKEARN J P.
PA (OLIN/) OLINS P O.
PA (PAIK/) PAIK K.
PA (THOM/) THOMAS J W.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2004-096775/10.
XX
PT Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating
PT aplastic anemia, involves culturing the stem cells with growth medium
PT comprising chimera protein, and harvesting the cultured stem cells.
XX
PS Disclosure; SEQ ID NO 176; 202pp; English.
XX
CC The invention relates to a novel method whereby stem cells are ex vivo
CC expanded via culturing the stem cells with a growth medium comprising a
CC chimera protein, followed by harvesting of the cultured stem cells. The
CC method of the invention has antianaemic, immunostimulant,
CC immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC cytostatic and neuroprotective applications and may be useful to target
CC haemopoietic cells for gene therapy, preferably for treating patients
CC having a haemopoietic disorder characterised by decreased levels of
CC myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC system. The expanded ex vivo cells may be used to treat neutropenia,
CC aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC myelofibrosis. The current sequence is that of a DNA related to the human
CC interleukin-3 (IL-3) mutant protein of the invention.
XX
SQ Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

Query Match 61.8%; Score 283; DB 12; Length 402;
Best Local Similarity 83.2%; Pred. No. 2.1e-42;
Matches 322; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Qy         52 ATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATC 111
              ||||| || || ||   |||| |||||| ||||||||||||||| |||||||| || |||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy        112 CAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACC 171
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Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy        172 GTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTC 231
              || || ||||| || || ||||| || ||||||||||||||| ||||| ||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy        232 GAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATG 291
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Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy        292 ATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAG 351
              |||||   |||||||||||||||||||| || |||||||| || ||||| || ||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        352 ATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTC 411
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Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        412 GACTGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||| || |||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAGTGA 387
```

RESULT 15
AAQ97183
ID AAQ97183 standard; DNA; 822 BP.
XX
AC AAQ97183;
XX
DT 25-AUG-1999 (first entry)
XX
DE pMON13035 DNA encoding IL-3 fusion protein.
XX
KW Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW mutant; mutein; fusion protein; linker; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9521254-A1.
XX
PD 10-AUG-1995.
XX
PF 02-FEB-1995; 95WO-US001185.
XX
PR 04-FEB-1994; 94US-00192325.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 1995-283774/37.
DR P-PSDB; AAR79320.
XX
PT Fusion proteins comprising a human interleukin-3 variant, a linker and
PT interleukin-3, a variant or a colony stimulating factor - useful to
PT increase haematopoietic cell prodn. in a mammal.
XX
PS Claim 22; Page 167-168; 447pp; English.
XX
CC A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC or IL-3 variant, and L is a linker. Generic sequences are described in
CC AAW03235 - AAW03242, and specifically claimed examples are shown in
CC AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC recombinant DNA techniques. Specifically claimed examples of DNA
CC sequences (including the present sequence) which encode these proteins
CC are shown in AAQ97167-Q97204 and AAQ97222-Q97227. The fusion protein is
CC used to increase haematopoietic cell production. It is also useful as an
CC IL-3 antagonist or as a discrete antigenic fragment for production of
CC antibodies useful in immunoassays and immunotherapy. Antagonists are used
CC to block the growth of certain cancer cells and in treatment of asthma.
CC The fusion protein can also be used to stimulate bone marrow and blood
CC cell activation and growth in vitro before infusion; and to treat
CC diseases characterised by decreased levels of myeloid, erythroid,
CC lymphoid and/or megakaryocyte cells of the haematopoietic system. The
CC protein has the usual activity of both its component proteins, but may

CC have increased synergistic activity and reduced undesired side effects
XX
SQ Sequence 822 BP; 222 A; 244 C; 180 G; 176 T; 0 U; 0 Other;

Query Match 61.4%; Score 281; DB 2; Length 822;
Best Local Similarity 83.1%; Pred. No. 4.8e-42;
Matches 320; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Qy        111 CCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGAC 170
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Db        498 CCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAAC 557

Qy        171 CGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCT 230
              || || ||||| || || ||||| || |||||||||||||| ||||| ||||||||||
Db        558 AGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCT 617

Qy        231 CGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCAT 290
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Qy        291 GATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCA 350
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Db        678 GATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCA 737

Qy        351 GATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTT 410
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Db        738 GATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTT 797

Qy        411 CGACTGCTGGGAGCCGGTGCAGGAG 435
              |||||||||||||| || ||||||
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Perfect score: 458
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Scoring table: IDENTITY_NUC
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Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	318.6	69.6	429	19	US-10-723-083-3	Sequence 3, Appli
3	312.6	68.3	435	17	US-10-188-056-31	Sequence 31, Appl
4	311	67.9	435	17	US-10-188-056-33	Sequence 33, Appl
5	283.6	61.9	777	16	US-10-083-446-55	Sequence 55, Appl
6	283	61.8	402	16	US-10-083-446-176	Sequence 176, App
7	281	61.4	822	16	US-10-083-446-69	Sequence 69, Appl
8	281	61.4	903	16	US-10-083-446-66	Sequence 66, Appl
9	277	60.5	2211	17	US-10-609-346-9	Sequence 9, Appli
10	276.8	60.4	448	17	US-10-609-346-19	Sequence 19, Appl
11	276.8	60.4	781	17	US-10-447-315-20	Sequence 20, Appl
12	276.8	60.4	789	16	US-10-131-985-16	Sequence 16, Appl
13	276.8	60.4	789	19	US-10-901-417-16	Sequence 16, Appl
14	276.2	60.3	1011	13	US-10-044-090-509	Sequence 509, App
15	275.8	60.2	435	9	US-09-826-025-8	Sequence 8, Appli
16	275.8	60.2	435	14	US-10-083-590-14	Sequence 14, Appl
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18	275.8	60.2	435	17	US-10-411-026-17	Sequence 17, Appl
19	275.8	60.2	435	17	US-10-410-962-17	Sequence 17, Appl
20	275.8	60.2	435	17	US-10-411-049-17	Sequence 17, Appl
21	275.8	60.2	435	18	US-10-410-930-17	Sequence 17, Appl
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27	275.8	60.2	435	19	US-10-410-980-17	Sequence 17, Appl
28	275.2	60.1	505	18	US-10-688-845-82	Sequence 82, Appl
29	275.2	60.1	737	15	US-10-081-969-19	Sequence 19, Appl
30	275.2	60.1	756	15	US-10-177-390-21	Sequence 21, Appl
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33	275.2	60.1	756	17	US-10-429-802-32	Sequence 32, Appl
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45	274.2	59.9	496	16	US-10-267-384-191	Sequence 191, App

ALIGNMENTS

RESULT 1
US-10-723-083-1
; Sequence 1, Application US/10723083
; Publication No. US20050050602A1
; GENERAL INFORMATION:
; APPLICANT: Altosaar, Illimar
; APPLICANT: Sardana, Ravinder
; APPLICANT: Dudani, Aail
; APPLICANT: Ganz, Peter
; APPLICANT: Tackaberry, Eilleen
; TITLE OF INVENTION: Production of GM-CSF in Plants
; FILE REFERENCE: 08-898901US
; CURRENT APPLICATION NUMBER: US/10/723,083
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: Canada 2,410,702
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (10)..(438)
; OTHER INFORMATION:
US-10-723-083-1

Query Match 100.0%; Score 458; DB 19; Length 458;
Best Local Similarity 100.0%; Pred. No. 7.2e-110;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        241 AAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCC 300
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Qy        301 CACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACC 360
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RESULT 2
US-10-723-083-3
; Sequence 3, Application US/10723083
; Publication No. US20050050602A1
; GENERAL INFORMATION:
; APPLICANT: Altosaar, Illimar
; APPLICANT: Sardana, Ravinder
; APPLICANT: Dudani, Aail
; APPLICANT: Ganz, Peter
; APPLICANT: Tackaberry, Eilleen
; TITLE OF INVENTION: Production of GM-CSF in Plants
; FILE REFERENCE: 08-898901US
; CURRENT APPLICATION NUMBER: US/10/723,083
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: Canada 2,410,702
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 429
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(429)
; OTHER INFORMATION:
US-10-723-083-3

Query Match 69.6%; Score 318.6; DB 19; Length 429;
Best Local Similarity 83.9%; Pred. No. 1.6e-73;
Matches 360; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

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Qy         10 ATGCACCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGC 69
              |||||||||||||||||||||||||||||||||||||||||||||||||| || || ||
Db          1 ATGCACCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCACCCGCCCGGTCA 60

Qy         70 CCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTC 129
              || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |||
Db         61 CCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTCTC 120

Qy        130 CTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAG 189
              || |||||     | ||||| || || |||||||| || || || || ||||| || ||
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Db        121 CTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTGATATCAGAA 180

Qy        190 ATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGC 249
              ||||| || |||||||||||||| ||||| |||||||||| ||||||||||||||||||||
Db        181 ATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGC 240

Qy        250 CTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACAAG 309
              || || |||||||||||||||||||||||| | ||||||||||   ||||||||||
Db        241 CTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACAAG 300

Qy        310 CAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGC 369
              |||||||||| || |||||||| || ||||| || |||||||| |||||||| || ||
Db        301 CAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGT 360

Qy        370 TTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTG 429
              ||||| |||||||| |||||||||| || || ||||| || ||||||||||||||| ||
Db        361 TTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTC 420

Qy        430 CAGGAGTGA 438
              |||||||||
Db        421 CAGGAGTGA 429
```

RESULT 3
US-10-188-056-31
; Sequence 31, Application US/10188056
; Publication No. US20040009934A1
; GENERAL INFORMATION:
; APPLICANT: Qiu, Jian-Tai
; APPLICANT: Lai, Wan-Ching
; APPLICANT: Chu, Yong Liang
; APPLICANT: Li, Frank Q.
; TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
; FILE REFERENCE: 3781-004-27
; CURRENT APPLICATION NUMBER: US/10/188,056
; CURRENT FILING DATE: 2002-09-26
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-188-056-31

Query Match 68.3%; Score 312.6; DB 17; Length 435;
Best Local Similarity 82.8%; Pred. No. 5.7e-72;
Matches 357; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

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Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  | ||  |   | |||    |    ||  ||  || || ||  | |
Db          5 GGCTGCAGAGCCTGCTCCTGCTGGGCACCGTGGCCTGCAGCATCAGCGCTCCCGCCAGAA 64

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
              |||| ||||| |||||||||| |||||||||||||||| |||||||||||| |  |||
Db         65 GCCCCAGCCCCTCCACCCAGCCCTGGGAGCACGTGAACGCCATCCAGGAGGCCAGACGGC 124

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              | || ||||| ||| | ||||||||||||||||||||||||||||||||||||||  ||
Db        125 TGCTGAACCTGTCCAGAGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCAGCG 184

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              |||||||||| || |||||||| ||||| || |||||||| || ||||||||||||||||
Db        185 AGATGTTCGACCTGCAGGAGCCCACCTGTCTGCAGACCCGGCTGGAGCTGTACAAGCAGG 244

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              | || || |||||||| |||||||| ||||| || || ||||||||||   ||||||||
Db        245 GACTGCGGGGCAGCCTGACCAAGCTGAAGGGACCCCTGACCATGATGGCCAGCCACTACA 304

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || || || |||||||  ||||||||||||||||||||||||||||||
Db        305 AGCAGCACTGCCCTCCCACACCCGAGACCAGCTGCGCCACCCAGATCATCACCTTCGAGA 364

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
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                ||||||||||||||||| |||||||||| || |||||||| |||||||||||||||| |
Db        365 GCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGACTGCTGGGAGCCCG 424

Qy        428 TGCAGGAGTGA 438
              ||||||||||
Db        425 TGCAGGAGTGA 435


RESULT 4
US-10-188-056-33
; Sequence 33, Application US/10188056
; Publication No. US20040009934A1
; GENERAL INFORMATION:
;  APPLICANT: Qiu, Jian-Tai
;  APPLICANT:  Lai, Wan-Ching
;  APPLICANT:  Chu, Yong Liang
;  APPLICANT:  Li, Frank Q.
;  TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
;  FILE REFERENCE: 3781-004-27
;  CURRENT APPLICATION NUMBER: US/10/188,056
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-188-056-33

  Query Match             67.9%;  Score 311;  DB 17;  Length 435;
  Best Local Similarity   82.6%;  Pred. No. 1.5e-71;
  Matches  356;  Conservative    0;  Mismatches   75;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  | ||  |    | |||   |    ||  ||  || || ||  | |
Db          5 GGCTGCAGAGCCTGCTCCTGCTGGGCACCGTGGCCTGCAGCATCAGCGCTCCCGCCAGAA 64

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
              |||| ||||| |||||||||||| |||||||||||||||||| |||||||||||| |  |||
Db         65 GCCCCAGCCCCTCCACCCAGCCCTGGGAGCACGTGAACGCCATCCAGGAGGCCAGACGGC 124

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              | || ||||| ||| | |||||||||||||||||||||||||||||||||||||||  ||
Db        125 TGCTGAACCTGTCCAGAGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCAGCG 184

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              |||||||||| || |||||||| ||||| || |||||||| || ||||||||||||||||
Db        185 AGATGTTCGACCTGCAGGAGCCCACCTGTCTGCAGACCCGGCTGGAGCTGTACAAGCAGG 244

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              | || || |||||||| |||||||| ||||| || || ||||||||||   ||||||||
Db        245 GACTGCGGGGCAGCCTGACCAAGCTGAAGGGACCCCTGACCATGATGGCCAGCCACTACA 304

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || || || ||||||  ||||||||||||| ||||||||||||||||
Db        305 AGCAGCACTGCCCTCCCACACCCGAGACCAGCTGCGCCACCCAGACCATCACCTTCGAGA 364

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              |||||||||||||||| |||||||||| || |||||||| |||||||||||||||||| |
Db        365 GCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGACTGCTGGGAGCCCG 424

Qy        428 TGCAGGAGTGA 438
              ||||||||||
Db        425 TGCAGGAGTGA 435


RESULT 5
US-10-083-446-55
; Sequence 55, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Thomas, John W.
;        TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                            Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;        NUMBER OF SEQUENCES: 197
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                        Corporate Patent Dept., Mail Zone O4E
;             STREET: 800 N. Lindbergh
;             CITY: St. Louis
;             STATE: Missouri
;             COUNTRY: USA
;             ZIP: 63167
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/083,446
;             FILING DATE: 26-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/762,227
;             FILING DATE: 09-DEC-1996
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: S. Christopher Bauer
;             REGISTRATION NUMBER: 42,305
;             REFERENCE/DOCKET NUMBER: C-2790/6
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (636)737-6257
;             TELEFAX: (636)737-5452
;    INFORMATION FOR SEQ ID NO: 55:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 777 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-083-446-55

  Query Match             61.9%;  Score 283.6;  DB 16;  Length 777;
  Best Local Similarity   81.6%;  Pred. No. 2e-64;
  Matches  328;  Conservative    0;  Mismatches   74;  Indels    0;  Gaps    0;

Qy         34 TCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGG 93
              || |||  ||    |  |||||| || || ||   ||||  |||||| ||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         94 GAGCACGTGAACGCGATCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCC 153
              || |||||||| || ||||||||||||||  | ||||| |||||     | ||||| ||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy        154 GCCGAGATGAACGAGACCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACC 213
              || ||||||||| || || || || ||||| || || ||||| || ||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy        214 TGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTC 273
              ||||| |||||||||| |||||||||||||||||||| || ||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy        274 AAGGGCCCGCTCACCATGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAG 333
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              |||||||| | ||||||||||| |||||||||||||||||||| || ||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        334 ACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTC 393
              || ||||| || |||||||| |||||||| || || ||||| |||||||| |||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        394 CTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTGCAGGAG 435
              || || || ||||| || |||||||||||||| || ||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777


RESULT 6
US-10-083-446-176
; Sequence 176, Application US/10083446
; Publication No. US20030185790A1
;  GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
;                  Caparon, Maire H.
;                  Easton, Alan M.
;                  Klein, Barbara K.
;                  McKearn, John P.
;                  Olins, Peter O.
;                  Paik, Kumnan
;                  Thomas, John W.
;       TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                           Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                       Corporate Patent Dept., Mail Zone O4E
;            STREET: 800 N. Lindbergh
;            CITY: St. Louis
;            STATE: Missouri
;            COUNTRY: USA
;            ZIP: 63167
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/083,446
;            FILING DATE: 26-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/762,227
;            FILING DATE: 09-DEC-1996
;            APPLICATION NUMBER: US 08/192,325
;            FILING DATE: 14-FEB-1994
;            APPLICATION NUMBER: US 08/446,872
;            FILING DATE: 06-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: S. Christopher Bauer
;            REGISTRATION NUMBER: 42,305
;            REFERENCE/DOCKET NUMBER: C-2790/6
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (636)737-6257
;            TELEFAX: (636)737-5452
;  INFORMATION FOR SEQ ID NO: 176:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 402 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 176:
US-10-083-446-176

  Query Match           61.8%;  Score 283;  DB 16;  Length 402;
  Best Local Similarity  83.2%;  Pred. No. 3e-64;
  Matches  322;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy         52 ATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATC 111
              ||||| || || ||   ||||  |||||| |||||||||||||| |||||||| || |||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy        112 CAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACC 171
              |||||||||||  | ||||| |||||     | ||||| || || ||||||||| || ||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy        172 GTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTC 231
              || || ||||| || || ||||| || ||||||||||||||| ||||| ||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy        232 GAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATG 291
              |||||||||||||||||| || |||||||||||||||||||||||||  | ||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy        292 ATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAG 351
              |||||  |||||||||||||||||||| || |||||||| || ||||| || ||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        352 ATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTC 411
              || |||||||| || || ||||| |||||||| |||||||||| || || ||||| ||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        412 GACTGCTGGGAGCCGGTGCAGGAGTGA 438
              |||||||||||||| || |||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAGTGA 387


RESULT 7
US-10-083-446-69
; Sequence 69, Application US/10083446
; Publication No. US20030185790A1
;  GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
;                  Caparon, Maire H.
;                  Easton, Alan M.
;                  Klein, Barbara K.
;                  McKearn, John P.
;                  Olins, Peter O.
;                  Paik, Kumnan
;                  Thomas, John W.
;       TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                           Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                       Corporate Patent Dept., Mail Zone O4E
;            STREET: 800 N. Lindbergh
;            CITY: St. Louis
;            STATE: Missouri
;            COUNTRY: USA
;            ZIP: 63167
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/083,446
;            FILING DATE: 26-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/762,227
;            FILING DATE: 09-DEC-1996
;            APPLICATION NUMBER: US 08/192,325
;            FILING DATE: 14-FEB-1994
;            APPLICATION NUMBER: US 08/446,872
;            FILING DATE: 06-JUN-1995
```

```
;       ATTORNEY/AGENT INFORMATION:
;            NAME: S. Christopher Bauer
;            REGISTRATION NUMBER: 42,305
;            REFERENCE/DOCKET NUMBER: C-2790/6
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (636)737-6257
;            TELEFAX: (636)737-5452
;   INFORMATION FOR SEQ ID NO: 69:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 822 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-083-446-69

  Query Match           61.4%;  Score 281;  DB 16;  Length 822;
  Best Local Similarity   83.1%;  Pred. No. 9.7e-64;
  Matches  320;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy         51 CATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGAT 110
              |||||| || || ||   ||||  |||||| |||||||||||||| |||||||| || ||
Db        438 CATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCAT 497

Qy        111 CCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGAC 170
              |||||||||||  | ||||| |||||     | ||||| || || |||||||| || ||
Db        498 CCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAAC 557

Qy        171 CGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCT 230
              || || ||||| || || ||||| || |||||||||||||| ||||| ||||||||||
Db        558 AGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCT 617

Qy        231 CGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCAT 290
              |||||||||||||||||||| || |||||||||||||||||||||||||  | |||||
Db        618 GGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCAT 677

Qy        291 GATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCA 350
              ||||||   |||||||||||||||||||| || |||||||| || ||||| || |||||
Db        678 GATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCA 737

Qy        351 GATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTT 410
              ||| |||||||| || || ||||| |||||||| |||||||||| || || ||||| ||
Db        738 GATTATCACCTTTGAAAGTTTCAAAGAAACCTGAAGGACTTCCTGCTTGTCATCCCCTT 797

Qy        411 CGACTGCTGGGAGCCGGTGCAGGAG 435
              |||||||||||||| || ||||||
Db        798 TGACTGCTGGGAGCCAGTCCAGGAG 822


RESULT 8
US-10-083-446-66
; Sequence 66, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
;                  Caparon, Maire H.
;                  Easton, Alan M.
;                  Klein, Barbara K.
;                  McKearn, John P.
;                  Olins, Peter O.
;                  Paik, Kumnan
;                  Thomas, John W.
;       TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                           Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                       Corporate Patent Dept., Mail Zone O4E
;            STREET: 800 N. Lindbergh
;            CITY: St. Louis
;            STATE: Missouri
;            COUNTRY: USA
;            ZIP: 63167
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/083,446
;            FILING DATE: 26-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/762,227
;            FILING DATE: 09-DEC-1996
;            APPLICATION NUMBER: US 08/192,325
;            FILING DATE: 14-FEB-1994
;            APPLICATION NUMBER: US 08/446,872
;            FILING DATE: 06-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: S. Christopher Bauer
;            REGISTRATION NUMBER: 42,305
;            REFERENCE/DOCKET NUMBER: C-2790/6
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (636)737-6257
;            TELEFAX: (636)737-5452
;   INFORMATION FOR SEQ ID NO: 66:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 903 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-083-446-66

  Query Match           61.4%;  Score 281;  DB 16;  Length 903;
  Best Local Similarity   83.1%;  Pred. No. 9.7e-64;
  Matches  320;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy         51 CATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGAT 110
              |||||| || || ||   ||||  |||||| |||||||||||||| |||||||| || ||
Db        519 CATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCAT 578

Qy        111 CCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGAC 170
              |||||||||||  | ||||| |||||     | ||||| || || |||||||| || ||
Db        579 CCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAAC 638

Qy        171 CGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCT 230
              || || ||||| || || ||||| || |||||||||||||| ||||| ||||||||||
Db        639 AGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCT 698

Qy        231 CGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCAT 290
              |||||||||||||||||||| || |||||||||||||||||||||||||  | |||||
Db        699 GGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCAT 758

Qy        291 GATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCA 350
              ||||||   |||||||||||||||||||| || |||||||| || ||||| || |||||
Db        759 GATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCA 818

Qy        351 GATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTT 410
              ||| |||||||| || || ||||| |||||||| |||||||||| || || ||||| ||
Db        819 GATTATCACCTTTGAAAGTTTCAAAGAAACCTGAAGGACTTCCTGCTTGTCATCCCCTT 878

Qy        411 CGACTGCTGGGAGCCGGTGCAGGAG 435
              |||||||||||||| || ||||||
Db        879 TGACTGCTGGGAGCCAGTCCAGGAG 903


RESULT 9
US-10-609-346-9
; Sequence 9, Application US/10609346
; Publication No. US20040063635A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Yu, Zailin
;  APPLICANT:  Fu, Yan
;  TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLO
;  TITLE OF INVENTION:  EFFECTS
;  FILE REFERENCE: ZYU-0603
;  CURRENT APPLICATION NUMBER: US/10/609,346
;  CURRENT FILING DATE:  2003-06-26
;  PRIOR APPLICATION NUMBER: US 60/392,948
;  PRIOR FILING DATE: 2002-07-01
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 2211
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA of HSA-GMCSF
US-10-609-346-9

  Query Match             60.5%;  Score 277;  DB 17;  Length 2211;
  Best Local Similarity   82.0%;  Pred. No. 1.1e-62;
  Matches  319;  Conservative    0;  Mismatches   70;  Indels    0;  Gaps    0;

Qy         50 GCATGGCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGA 109
              || | || || || |||   || |||||   ||| ||||| |||||||| ||||| || |
Db       1823 GCTTAGCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCA 1882

Qy        110 TCCAGGAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGA 169
              |||||||||||||  | |||||  |||||      | |||||  || || |||||||| || |
Db       1883 TCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAA 1942

Qy        170 CCGTGGAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCC 229
              | || || || ||||| || ||||| || |||||||||||||||||||| |||||||||
Db       1943 CAGTAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCC 2002

Qy        230 TCGAGCTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCA 289
              | |||||||||||||||||||| || ||||||||||||||||||||||||  | ||||
Db       2003 TGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCA 2062

Qy        290 TGATGGCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCC 349
              |||||||   |||||||||||||||||||| || |||||||| || ||||| || ||||
Db       2063 TGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCC 2122

Qy        350 AGATCATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGT 409
              |||| |||||||| || || ||||| |||||||| |||||||| || || || ||||| |
Db       2123 AGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCT 2182

Qy        410 TCGACTGCTGGGAGCCGGTGCAGGAGTGA 438
              | |||||||||||||| || |||||||||
Db       2183 TTGACTGCTGGGAGCCAGTCCAGGAGTGA 2211


RESULT 10
US-10-609-346-19
; Sequence 19, Application US/10609346
; Publication No. US20040063635A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Zailin
;  APPLICANT:  Fu, Yan
;  TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLO
;  TITLE OF INVENTION:  EFFECTS
;  FILE REFERENCE: ZYU-0603
;  CURRENT APPLICATION NUMBER: US/10/609,346
;  CURRENT FILING DATE:  2003-06-26
;  PRIOR APPLICATION NUMBER: US 60/392,948
;  PRIOR FILING DATE: 2002-07-01
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
;   LENGTH: 448
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-609-346-19

  Query Match             60.4%;  Score 276.8;  DB 17;  Length 448;
  Best Local Similarity   77.5%;  Pred. No. 1.2e-62;
  Matches  335;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||  ||  |  | |    | | |    |   ||  |  || || || |||
Db          5 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 64

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
              || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db         65 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 124

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || ||||| |
Db        125 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 184

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        185 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 244

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||||| | ||||||||||   ||||||||
Db        245 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 304

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        305 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 364

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || ||||||||||||||| |
Db        365 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 424

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        425 TCCAGGAGTGAG 436


RESULT 11
US-10-447-315-20
; Sequence 20, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
;  APPLICANT: Rafii, Shahin
;  APPLICANT:  Heissig, Beate
;  APPLICANT:  Hattori, Koichi
;  APPLICANT:  Cornell Research Foundation, Inc.
;  TITLE OF INVENTION: Adult Stem Cell Recruitment
;  FILE REFERENCE: 1676.006US1
;  CURRENT APPLICATION NUMBER: US/10/447,315
;  CURRENT FILING DATE:  2003-05-28
;  PRIOR APPLICATION NUMBER: US 60/383,658
;  PRIOR FILING DATE: 2002-05-28
;  NUMBER OF SEQ ID NOS: 28
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 781
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-447-315-20

  Query Match             60.4%;  Score 276.8;  DB 17;  Length 781;
  Best Local Similarity   77.5%;  Pred. No. 1.2e-62;
  Matches  335;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||  ||  |  | |    | | |    |   ||  |  || || || |||
Db         37 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 96

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
              || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db         97 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 156
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Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || || ||||| |
Db        157 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 216

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        217 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 276

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||||  | ||||||||||   ||||||||
Db        277 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 336

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        337 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 396

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || ||||||||||||| |
Db        397 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 456

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        457 TCCAGGAGTGAG 468
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RESULT 12
US-10-131-985-16
; Sequence 16, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-985-16

Query Match 60.4%; Score 276.8; DB 16; Length 789;
Best Local Similarity 77.5%; Pred. No. 1.2e-62;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

```
Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |     | | |    |   ||  |  || || || |||
Db         37 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 96

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| ||||| |||||||| ||||| || |||||||||||||  | |
Db         97 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 156

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || || ||||| |
Db        157 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 216

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        217 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 276
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Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||||  | ||||||||||   ||||||||
Db        277 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 336

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        337 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 396

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || ||||||||||||| |
Db        397 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 456

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        457 TCCAGGAGTGAG 468
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RESULT 13
US-10-901-417-16
; Sequence 16, Application US/10901417
; Publication No. US20050026836A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Occleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/901,417
; CURRENT FILING DATE: 2004-07-28
; PRIOR APPLICATION NUMBER: US/10/131,985
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-901-417-16

Query Match 60.4%; Score 276.8; DB 19; Length 789;
Best Local Similarity 77.5%; Pred. No. 1.2e-62;
Matches 335; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

```
Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |     | | |    |   ||  |  || || || |||
Db         37 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 96

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| ||||| |||||||| ||||| || |||||||||||||  | |
Db         97 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 156

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || || ||||| |
Db        157 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 216

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        217 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 276

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||||||||  | ||||||||||   ||||||||
Db        277 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 336

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        337 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 396
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Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || ||||||||||||||| |
Db        397 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 456

Qy        428 TGCAGGAGTGAG 439
              | ||||||||||
Db        457 TCCAGGAGTGAG 468


RESULT 14
US-10-044-090-509
; Sequence 509, Application US/10044090
; Publication No. US20020137081A1
; GENERAL INFORMATION:
;  APPLICANT: Olga Bandman
;  TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
;  FILE REFERENCE: PA-0028 US
;  CURRENT APPLICATION NUMBER: US/10/044,090
;  CURRENT FILING DATE:  2002-01-09
;  NUMBER OF SEQ ID NOS: 850
;  SOFTWARE: PERL Program
; SEQ ID NO 509
;   LENGTH: 1011
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: Incyte ID No. US20020137081A1 370489.47
US-10-044-090-509

  Query Match             60.3%;  Score 276.2;  DB 13;  Length 1011;
  Best Local Similarity   82.3%;  Pred. No. 1.7e-62;
  Matches  317;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy         55 GCGCCAGCGCGCAGCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAG 114
              || || || |||   || |||||   ||| ||||| |||||||| ||||| || ||||||
Db         87 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 146

Qy        115 GAGGCCCGCAGGCTCCTCAACCTCTCCCGCGACACCGCCGCCGCGAGATGAACGAGACCGTG 174
              ||||||||  | ||||| |||||     | ||||| || || |||||||| || || ||
Db        147 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 206

Qy        175 GAGGTGATCTCCGAGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAG 234
              || || ||||| || ||||| || |||||||||||||||||||| |||||||||| |||
Db        207 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 266

Qy        235 CTGTACAAGCAGGGCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATG 294
              |||||||||||||||| || |||||||||||||||||||||||||| | |||||||||
Db        267 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 326

Qy        295 GCGTCCCACTACAAGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATC 354
              ||   |||||||||||||||||||| || |||||||| || ||||| || ||||||||
Db        327 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 386

Qy        355 ATCACCTTCGAGAGCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGAC 414
              |||||||| || || ||||| |||||||| |||||||| || || || ||||| || |||
Db        387 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 446

Qy        415 TGCTGGGAGCCGGTGCAGGAGTGAG 439
              |||||||||||| || ||||||||||
Db        447 TGCTGGGAGCCAGTCCAGGAGTGAG 471


RESULT 15
US-09-826-025-8
; Sequence 8, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 435 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-826-025-8

  Query Match             60.2%;  Score 275.8;  DB 9;  Length 435;
  Best Local Similarity   77.5%;  Pred. No. 2.2e-62;
  Matches  334;  Conservative    0;  Mismatches   97;  Indels    0;  Gaps    0;

Qy          8 GGATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCGCCAGCGCGCA 67
              || ||||   ||  |  | |      | | |    |    ||  |   || || || |||
Db          5 GGCTGCAGAGCCTGCTGCTCTTGGGCACTGTGGCCTGCAGCATCTCTGCACCCGCCCGCT 64

Qy         68 GCCCGAGCCCGTCCACCCAGCCGTGGGAGCACGTGAACGCGATCCAGGAGGCCCGCAGGC 127
                || |||||   ||| ||||| |||||||| ||||| || ||||||||||||||  | |
Db         65 CGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTC 124

Qy        128 TCCTCAACCTCTCCCGCGACACCGCCGCCGAGATGAACGAGACCGTGGAGGTGATCTCCG 187
              |||| |||||     | ||||| || || |||||||| || || || || || ||||| |
Db        125 TCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAG 184

Qy        188 AGATGTTCGATCTCCAGGAGCCGACCTGCCTCCAGACCCGCCTCGAGCTGTACAAGCAGG 247
              | ||||| || |||||||||||||||||||| |||||||||| ||||||||||||||||
Db        185 AAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGG 244

Qy        248 GCCTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACA 307
              |||| || |||||||||||||||||||| | ||||||||||    ||||||||
Db        245 GCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACA 304

Qy        308 AGCAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGA 367
              |||||||||||| || |||||||| || ||||| || |||||||| |||||||| || |
Db        305 AGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAA 364

Qy        368 GCTTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGG 427
              | ||||| |||||||| |||||||| || || || ||||| || |||||||||||||| |
Db        365 GTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAG 424

Qy        428 TGCAGGAGTGA 438
              | |||||||||
Db        425 TCCAGGAGTGA 435
```

Search completed: March 11, 2005, 18:28:48
Job time : 457 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2005, 17:24:26 ; Search time 473 Seconds
(without alignments)
1777.174 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHHHSSGIEGRMAPARS.....ENLKDFLLVIPFDCWEPVQE 142

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10723083/runat_08032005_131715_10414/app_query.fasta_1.327
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10723083_@CGN_1_1_644_@runat_08032005_131715_10414 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	682	89.2	777	2	AAQ97169	Aaq97169 pMON13022
2	682	89.2	777	3	AAA03723	Aaa03723 Human int
3	682	89.2	777	6	ABX00012	Abx00012 Human int
4	682	89.2	777	12	ADJ14267	Adj14267 DNA relat
5	679	88.8	1610	2	AAT72724	Aat72724 p53-GM-CS
6	678	88.6	384	2	AAT34400	Aat34400 Granulocy
7	678	88.6	384	2	ABA96672	Aba96672 Human gra
8	678	88.6	402	2	AAQ97208	Aaq97208 pMON13012
9	678	88.6	402	3	AAA03771	Aaa03771 Human G-C
10	678	88.6	402	6	ABX00086	Abx00086 Human int
11	678	88.6	402	12	ADJ14388	Adj14388 DNA relat
12	678	88.6	410	1	AAN81322	Aan81322 Sequence
13	678	88.6	415	1	AAN90383	Aan90383 Synthetic
14	678	88.6	415	1	AAN90274	Aan90274 Synthetic
15	678	88.6	822	2	AAQ97183	Aaq97183 pMON13035
16	678	88.6	822	3	AAA03737	Aaa03737 Human int
17	678	88.6	822	6	ABX00026	Abx00026 Human int
18	678	88.6	822	12	ADJ14281	Adj14281 DNA relat
19	678	88.6	903	2	AAQ97180	Aaq97180 pMON13031
20	678	88.6	903	3	AAA03734	Aaa03734 Human int
21	678	88.6	903	6	ABX00023	Abx00023 Human int
22	678	88.6	903	12	ADJ14278	Adj14278 DNA relat
23	676	88.4	1630	3	AAZ50587	Aaz50587 HD70scFv-
24	675	88.2	2211	12	ADL16719	Adl16719 Human stu
25	673	88.0	381	3	AAZ88268	Aaz88268 Granulocy
26	673	88.0	384	2	AAT34399	Aat34399 Granulocy
27	673	88.0	410	1	AAN81320	Aan81320 Sequence
28	673	88.0	429	12	ADJ36194	Adj36194 Self-coal
29	673	88.0	435	2	AAV83189	Aav83189 Granulocy
30	673	88.0	435	3	AAA64392	Aaa64392 DNA seque
31	673	88.0	435	10	ADF15808	Adf15808 Human alb
32	673	88.0	435	10	ADF15714	Adf15714 Human alb
33	673	88.0	435	10	ADF15807	Adf15807 Human alb
34	673	88.0	435	10	ADF15715	Adf15715 Human alb
35	673	88.0	435	10	ACC78877	Acc78877 Human GM-
36	673	88.0	435	12	ADI20788	Adi20788 Human GM-
37	673	88.0	435	12	ADI20789	Adi20789 Human GM-
38	673	88.0	435	12	ADN49689	Adn49689 Human gra
39	673	88.0	435	12	ADQ76022	Adq76022 Human GM-
40	673	88.0	435	12	ADQ76023	Adq76023 Human GM-
41	673	88.0	440	1	AAN81321	Aan81321 Sequence
42	673	88.0	448	12	ADL16729	Adl16729 Human gra
43	673	88.0	505	13	ADS88046	Ads88046 Tumour tr
44	673	88.0	579	12	ADJ36238	Adj36238 Self-coal
45	673	88.0	661	1	AAN70561	Aan70561 Sequence

ALIGNMENTS

RESULT 1
AAQ97169
ID AAQ97169 standard; DNA; 777 BP.
XX
AC AAQ97169;
XX
DT 25-AUG-1999 (first entry)
XX
DE pMON13022 DNA encoding IL-3 fusion protein.
XX
KW Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW mutant; mutein; fusion protein; linker; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9521254-A1.
XX
PD 10-AUG-1995.
XX
PF 02-FEB-1995; 95WO-US001185.
XX
PR 04-FEB-1994; 94US-00192325.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX

```
DR   WPI; 1995-283774/37.
DR   P-PSDB; AAR79317.
XX
PT   Fusion proteins comprising a human interleukin-3 variant, a linker and
PT   interleukin-3, a variant or a colony stimulating factor - useful to
PT   increase haematopoietic cell prodn. in a mammal.
XX
PS   Claim 22; Page 158-159; 447pp; English.
XX
CC   A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC   R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC   interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC   including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC   or IL-3 variant, and L is a linker. Generic sequences are described in
CC   AAW03235 - AAW03242, and specifically claimed examples are shown in
CC   AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC   recombinant DNA techniques. Specifically claimed examples of DNA
CC   sequences (including the present sequence) which encode these proteins
CC   are shown in AAQ97167-Q97204 and AAQ97222-Q97227. The fusion protein is
CC   used to increase haematopoietic cell production. It is also useful as an
CC   IL-3 antagonist or as a discrete antigenic fragment for production of
CC   antibodies useful in immunoassays and immunotherapy. Antagonists are used
CC   to block the growth of certain cancer cells and in treatment of asthma.
CC   The fusion protein can also be used to stimulate bone marrow and blood
CC   cell activation and growth in vitro before infusion; and to treat
CC   diseases characterised by decreased levels of myeloid, erythroid,
CC   lymphoid and/or megakaryocyte cells of the haematopoietic system. The
CC   protein has the usual activity of both its component proteins, but may
CC   have increased synergistic activity and reduced undesired side effects
XX
SQ   Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.38e-67      Length:          777
Score:                    682.00        Matches:         130
Percent Similarity:       97.01%        Conservative:    0
Best Local Similarity:    97.01%        Mismatches:      4
Query Match:              89.15%        Indels:          0
DB:                       2             Gaps:            0

US-10-723-083-2 (1-142) x AAQ97169 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||          ||||||||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 2
AAA03723
ID   AAA03723 standard; DNA; 777 BP.
XX
AC   AAA03723;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human interleukin-3 mutant containing fusion protein DNA SEQ ID NO:55.
XX
KW   Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
KW   colony stimulating factor; haematopoietic growth factor; lymphokine;
KW   fusion protein; haematopoietic disorder; infection; cancer;
KW   radiation therapy; chemotherapy; bone marrow suppressive drug;
KW   bone marrow activation; blood cell activation; blood transplant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6022535-A.
XX
PD   08-FEB-2000.
XX
PF   06-JUN-1995;   95US-00469318.
XX
PR   04-FEB-1994;   94US-00192325.
PR   02-FEB-1995;   95WO-US001185.
PR   06-APR-1995;   95US-00411795.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer SC,  Abrams MA,  Braford-Goldberg SR,  Easton AM,  Klein BK;
PI   Paik K,  Thomas JW,  Mckearn JP,  Olins PO,  Caparon MH;
XX
DR   WPI; 2000-160368/14.
XX
PT   Treating hematopoietic disorders with fusion proteins comprising mutated
PT   interleukin-3 fused with secondary colony stimulating factors or other
PT   interleukin-3 variants.
XX
PS   Example 27; Col 135-136; 276pp; English.
XX
CC   Methods have been developed for treating haematopoietic disorders with
CC   fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-
CC   3) variants or mutant proteins (muteins) fused with secondary colony
CC   stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
CC   and/or haematopoietic colony stimulating factors) or other interleukin-3
CC   variants with or without a linker. The methods may be used in vivo to
CC   treat haematopoietic disorders resulting from bacterial, viral and fungal
CC   infections, cancer radiation therapy, chemotherapy or bone marrow
CC   suppressive drugs. They may also be used in vitro to stimulate bone
CC   marrow and blood cell activation and growth prior to infusion of the bone
CC   marrow and blood transplants into patients. IL-3 is a haematopoietic
CC   growth factor which has the property of being able to promote the
CC   survival, growth and differentiation of haematopoietic cells. The fusion
CC   molecules are characterised by possessing the usual activity of both of
CC   their constituent peptides and further by having a biological or
CC   physiological activity greater than the additive function of the IL-3 or
CC   second CSF alone (i.e. the peptides act synergistically). Their activity
CC   may also be further enhanced by the mutations they comprise. The
CC   variations may further reduce undesirable side effects associated with IL
CC   -3. AAY53130 to AAY53226, and AAA03721 to AAA03782 represent sequences
CC   used in the exemplification of the present invention
XX
SQ   Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.38e-67      Length:          777
Score:                    682.00        Matches:         130
Percent Similarity:       97.01%        Conservative:    0
Best Local Similarity:    97.01%        Mismatches:      4
Query Match:              89.15%        Indels:          0
DB:                       3             Gaps:            0

US-10-723-083-2 (1-142) x AAA03723 (1-777)
```

```
Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||           ||||||||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777
```

RESULT 3
ABX00012
ID ABX00012 standard; DNA; 777 BP.
XX
AC ABX00012;
XX
DT 18-DEC-2002 (first entry)
XX
DE Human interleukin-3 associated DNA sequence #3.
XX
KW Haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; ds;
KW G-CSF; G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
KW human growth hormone; B-cell growth factor; leukaemia;
KW B-cell differentiation factor; eosinophil differentiation factor;
KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
KW myelofibrosis; Interleukin-3; IL-3; stem cell.
XX
OS Unidentified.
XX
PN US6436387-B1.
XX
PD 20-AUG-2002.
XX
PF 09-DEC-1996; 96US-00762227.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 04-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2002-749206/81.
XX
PT Ex vivo expansion of stem cells, for enhancing transduction efficiency of
PT cultured stem cells, comprises culturing stem cells in growth medium
PT having mutant interleukin-3, and hematopoietic factor, and harvesting
PT cultured cells.
XX
PS Disclosure; Col 161-164; 203pp; English.
XX
CC The invention relates to ex vivo expansion of stem cells, comprises
CC culturing stem cells with a growth medium comprising a chimaera protein,
CC and harvesting the cultured stem cells. The chimaera is based on a
CC mutated human interleukin-3 (IL_3) sequence coupled to a haematopoietic
CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
CC CSFSer17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
CC differentiation factor, eosinophil differentiation factor and stem cell
CC factor (SCF)) via a peptide linker. The formula for the chimaera is given
CC in the specification. Also included is a method for enhancing the
CC efficiency of the transduction of cultured stem cells by a heterologous
CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
CC culturing the stem cells with a growth medium comprising the chimaera (c)
CC transducing DNA into cultured cells; and (d) harvesting the transduced
CC cells. The method is useful for ex vivo expansion of stem cells, and
CC enhancing the efficiency of the transduction of cultured stem cells by a
CC heterologous gene. The method is also useful for treating a patient
CC having a haematopoietic disorder. The expanded haematopoietic cells are
CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
CC and myelofibrosis. The present sequence is an IL-3 mutant associated DNA
CC sequence. Note: The present sequence is included in the sequence listing
CC but is not mentioned anywhere else in the specification
XX
SQ Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.38e-67	Length:	777
Score:	682.00	Matches:	130
Percent Similarity:	97.01%	Conservative:	0
Best Local Similarity:	97.01%	Mismatches:	4
Query Match:	89.15%	Indels:	0
DB:	6	Gaps:	0

US-10-723-083-2 (1-142) x ABX00012 (1-777)

```
Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||           ||||||||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777
```

RESULT 4
ADJ14267
ID ADJ14267 standard; DNA; 777 BP.
XX
AC ADJ14267;

```
XX
DT   20-MAY-2004  (first entry)
XX
DE   DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID 55.
XX
KW   stem cell; antianaemic; immunostimulant; immunomodulator;
KW   antiinflammatory; dermatological; immunosuppressive; cytostatic;
KW   neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;
KW   lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
KW   Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
KW   myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.
XX
OS   Unidentified.
XX
PN   US2003185790-A1.
XX
PD   02-OCT-2003.
XX
PF   26-FEB-2002; 2002US-00083446.
XX
PR   24-NOV-1992;   92US-00981044.
PR   22-NOV-1993;   93WO-US011197.
PR   04-FEB-1994;   94US-00192325.
PR   02-FEB-1995;   95WO-US001185.
PR   06-APR-1995;   95US-00411795.
PR   06-JUN-1995;   95US-00446872.
PR   09-DEC-1996;   96US-00762227.
XX
PA   (BAUE/) BAUER S C.
PA   (ABRA/) ABRAMS M A.
PA   (BRAF/) BRAFORD-GOLDBERG S R.
PA   (CAPA/) CAPARON M H.
PA   (EAST/) EASTON A M.
PA   (KLEI/) KLEIN B K.
PA   (MCKE/) MCKEARN J P.
PA   (OLIN/) OLINS P O.
PA   (PAIK/) PAIK K.
PA   (THOM/) THOMAS J W.
XX
PI   Bauer SC,  Abrams MA,  Braford-Goldberg SR,  Caparon MH,  Easton AM;
PI   Klein BK,  Mckearn JP,  Olins PO,  Paik K,  Thomas JW;
XX
DR   WPI; 2004-096775/10.
XX
PT   Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating
PT   aplastic anemia, involves culturing the stem cells with growth medium
PT   comprising chimera protein, and harvesting the cultured stem cells.
XX
PS   Disclosure; SEQ ID NO 55; 202pp; English.
XX
CC   The invention relates to a novel method whereby stem cells are ex vivo
CC   expanded via culturing the stem cells with a growth medium comprising a
CC   chimera protein, followed by harvesting of the cultured stem cells. The
CC   method of the invention has antianaemic, immunostimulant,
CC   immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC   cytostatic and neuroprotective applications and may be useful to target
CC   haemopoietic cells for gene therapy, preferably for treating patients
CC   having a haemopoietic disorder characterised by decreased levels of
CC   myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC   system. The expanded ex vivo cells may be used to treat neutropenia,
CC   aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC   systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC   myelofibrosis. The current sequence is that of a DNA related to the human
CC   interleukin-3 (IL-3) mutant protein of the invention.
XX
SQ   Sequence 777 BP; 204 A; 227 C; 183 G; 163 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.38e-67        Length:         777
Score:                  682.00          Matches:        130
Percent Similarity:     97.01%          Conservative:   0
Best Local Similarity:  97.01%          Mismatches:     4
Query Match:            89.15%          Indels:         0

DB:                     12              Gaps:           0

US-10-723-083-2 (1-142) x ADJ14267 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||                 ||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 5
AAT72724
ID   AAT72724 standard; cDNA; 1610 BP.
XX
AC   AAT72724;
XX
DT   17-SEP-1997  (first entry)
XX
DE   p53-GM-CSF immunostimulant fusion protein DNA.
XX
KW   p53-GM-CSF; granulocyte macrophage colony stimulating factor;
KW   tumour suppressor gene; immunostimulant; cancer; therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             9. .1610
FT                   /*tag=  a
FT                   /product= "p53-GM-CSF fusion protein"
FT   mRNA            9. .1187
FT                   /*tag=  b
FT                   /product= "p53"
FT   mRNA            1188. .1193
FT                   /*tag=  c
FT                   /product= "Ser-Arg linker"
FT   mRNA            1194. .1610
FT                   /*tag=  d
FT                   /product= "GM-CSF"
XX
PN   WO9724438-A1.
XX
PD   10-JUL-1997.
XX
PF   23-DEC-1996;   96WO-US020241.
XX
PR   28-DEC-1995;   95US-00579823.
XX
PA   (ACTI-) ACTIVATED CELL THERAPY INC.
XX
PI   Laus R,  Ruegg CL,  Wu H;
XX
```

```
DR   WPI; 1997-363674/33.
DR   P-PSDB; AAW19763.
XX
PT   Potent APC that activates T-cells to give multivalent cellular immune
PT   response - can also induce a cytotoxic T-cell response in a vertebrate
PT   subject.
XX
PS   Example 7; Fig 11; 45pp; English.
XX
CC   A nucleic acid molecule (AAT72724) codes for a fusion protein (AAW19763)
CC   comprising human p53 tumour suppressor protein and granulocyte-macrophage
CC   colony stimulating factor (GM-CSF). It was prepd. by PCR amplification of
CC   p53 cDNA GM-CSF cDNA sequences (the GM-CSF antisense primer including a
CC   hexahistidine tag sequence) and their fusion via a XbaI linker. Fusion
CC   expression vectors can be used to transfect mammalian and insect cells.
CC   The p53-GM-CSF fusion protein is used to generate anti-p53 immunity.
CC   Tumour cells are eliminated by cytotoxic T lymphocytes activated in vivo
CC   or in vitro by exposure to antigen-presenting cells exposed to the fusion
CC   protein
XX
SQ   Sequence 1610 BP; 383 A; 508 C; 407 G; 312 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              8.21e-67      Length:         1610
Score:                  679.00        Matches:        128
Percent Similarity:     98.47%        Conservative:   1
Best Local Similarity:  97.71%        Mismatches:     2
Query Match:            88.76%        Indels:         0
DB:                     2             Gaps:           0

US-10-723-083-2 (1-142) x AAT72724 (1-1610)

Qy         12 GluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisVal 31
              :::   |||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1185 GACTCTAGATCCGCACCCGCCCGCTCGCCCAGCCCCAGCACACAGCCCTGGGAGCATGTG 1244

Qy         32 AsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMet 51
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1245 AATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATG 1304

Qy         52 AsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGln 71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1305 AATGAAACAGTAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAG 1364

Qy         72 ThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyPro 91
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1365 ACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCC 1424

Qy         92 LeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCys 111
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1425 TTGACCATGATGGCCAGCCACTACAAACAGCACTGCCCTCCAACCCCGGAAACTTCCTGT 1484

Qy        112 AlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuVal 131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1485 GCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTC 1544

Qy        132 IleProPheAspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||||||||||
Db       1545 ATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 1577

RESULT 6
AAT34400
ID   AAT34400 standard; DNA; 384 BP.
XX
AC   AAT34400;
XX
DT   25-MAR-2003  (revised)
DT   11-FEB-1997  (first entry)
XX
DE   Granulocyte macrophage colony-stimulating factor coding sequence.
XX
KW   GM-CSF; granulocyte macrophage colony-stimulating factor; expression;
KW   construct; stable; production; ds.
XX
OS   Homo sapiens.
XX
PN   JP08173185-A.
XX
PD   09-JUL-1996.
XX
PF   28-APR-1987;   95JP-00263370.
XX
PR   28-APR-1987;   87JP-00106148.
XX
PA   (AMGE-) AMGEN INC.
PA   (KIRI ) KIRIN BREWERY KK.
XX
DR   WPI; 1996-365600/37..
DR   N-PSDB; AAW00103.
XX
PT   Prodn. of human granulocyte macrophage colony-stimulating factor - by
PT   culturing E. coli transformed with human GM-CSF DNA.
XX
PS   Claim 1; Page 2; 16pp; Japanese.
XX
CC   The present sequence encodes human granulocyte macrophage colony-
CC   stimulating factor (hGM-CSF; n = 101, Ile). A series of oligonucleotides
CC   were synthesised and ligated together to form a stable expression
CC   construct. The technique is used for the efficient prodn. of a
CC   glycoprotein with hGM-CSF activity. (Updated on 25-MAR-2003 to correct PF
CC   field.)
XX
SQ   Sequence 384 BP; 101 A; 100 C; 86 G; 97 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.5e-67       Length:         384
Score:                  678.00        Matches:        128
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            88.63%        Indels:         0
DB:                     2             Gaps:           0

US-10-723-083-2 (1-142) x AAT34400 (1-384)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCAGCTCGATCACCGTCCCCGTCCACTCAACCATGGGAACATGTTAACGCAATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAAGCTCGTCGTCTGCTGAACCTGTCTCGTGATACTGCTGCTGAAATGAACGAAACT 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTGAAGTGATCAGCGAAATGTTCGATCTGCAGGAACCGACTTGTCTGCAAACCCGTCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACTGTACAAACAAGGTCTGCGTGGTTCTCTGACTAAACTGAAAGGTCCGCTGACTATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCTAGCCATTACAAACAGCATTGTCCGCCGACTCCGGAAACTTCTTGTGCTACTCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATCATCACTTTCGAATCTTTCAAAGAAAACCTGAAAGATTTCCTGCTGGTTATCCCGTTC 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GATTGTTGGGAACCGGTTCAGGAA 384

RESULT 7
ABA96672
ID   ABA96672 standard; cDNA; 384 BP.
XX
```

```
AC   ABA96672;
XX
DT   23-APR-2002  (first entry)
XX
DE   Human granulocyte macrophage-colony stimulating factor (hGM-CSF) cDNA.
XX
KW   Human; GM-CSF; granulocyte macrophage-colony stimulating factor;
KW   recombinant production; Escherichia coli; pET-11d vector; gene; ds.
XX
OS   Homo sapiens.
XX
PN   KR98053420-A.
XX
PD   25-SEP-1998.
XX
PF   26-DEC-1996;   96KR-00072523.
XX
PR   26-DEC-1996;   96KR-00072523.
XX
PA   (CHEI-) CHEIL FOODS & CHEM INC.
XX
PI   Ahn DH,  Lee HS,  Mok H,  Hah SH,  Koh HG,  Oh MS,  Kim HS;
XX
DR   WPI; 1999-517067/43.
XX
PT   Human granulocyte macrophage-colony stimulating factor.
XX
PS   Example 1; Fig 4; 7pp; Korean.
XX
CC   The invention relates to the recombinant production of human granulocyte
CC   macrophage-colony stimulating factor (hGM-CSF). NcoI and BamHI
CC   restriction sites were inserted into hGM-CSF cDNA (ABA96672) via PCR
CC   using primers ABA96670-ABA96671, prior to cleavage with these enzymes and
CC   insertion into the pET-11d vector downstream of the T7/lac promoter to
CC   form the plasmid pT7GMCSF. pT7GMCSF was transformed into Escherichia coli
CC   BL21(DE3) pLysS for recombinant expression of hGM-CSF. The present
CC   sequence represents hGM-CSF cDNA
XX
SQ   Sequence 384 BP; 93 A; 125 C; 97 G; 69 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.5e-67       Length:          384
Score:                  678.00        Matches:         128
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            88.63%        Indels:          0
DB:                     2             Gaps:            0

US-10-723-083-2 (1-142) x ABA96672 (1-384)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 8
AAQ97208
ID   AAQ97208 standard; DNA; 402 BP.
XX
AC   AAQ97208;
XX
DT   25-AUG-1999  (first entry)
XX
DE   pMON13012 DNA sequence.
XX
KW   Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW   mutant; mutein; fusion protein; linker; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9521254-A1.
XX
PD   10-AUG-1995.
XX
PF   02-FEB-1995;   95WO-US001185.
XX
PR   04-FEB-1994;   94US-00192325.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer CS,  Abrams MA,  Braford-Goldberg SR,  Caparon MH,  Easton AM;
PI   Klein BK,  Mckearn JP,  Olins PO,  Paik K,  Thomas JW;
XX
DR   WPI; 1995-283774/37.
DR   P-PSDB; AAR79338.
XX
PT   Fusion proteins comprising a human interleukin-3 variant, a linker and
PT   interleukin-3, a variant or a colony stimulating factor - useful to
PT   increase haematopoietic cell prodn. in a mammal.
XX
PS   Example 19; Page 183; 447pp; English.
XX
CC   A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC   R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC   interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC   including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC   or IL-3 variant, and L is a linker. Generic sequences are described in
CC   AAW03235 - AAW03242, and specifically claimed examples are shown in
CC   AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC   recombinant DNA techniques. Specifically claimed examples of DNA
CC   sequences which encode these proteins are shown in AAQ97167-Q97204 and
CC   AAQ97222-Q97227. The fusion protein is used to increase haematopoietic
CC   cell production. It is also useful as an IL-3 antagonist or as a discrete
CC   antigenic fragment for production of antibodies useful in immunoassays
CC   and immunotherapy. Antagonists are used to block the growth of certain
CC   cancer cells and in treatment of asthma. The fusion protein can also be
CC   used to stimulate bone marrow and blood cell activation and growth in
CC   vitro before infusion; and to treat diseases characterised by decreased
CC   levels of myeloid, erythroid, lymphoid and/or megakaryocyte cells of the
CC   haematopoietic system. The protein has the usual activity of both its
CC   component proteins, but may have increased synergistic activity and
CC   reduced undesired side effects
XX
SQ   Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.59e-67      Length:          402
Score:                  678.00        Matches:         128
Percent Similarity:     100.00%       Conservative:    0
Best Local Similarity:  100.00%       Mismatches:      0
Query Match:            88.63%        Indels:          0
DB:                     2             Gaps:            0
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US-10-723-083-2 (1-142) x AAQ97208 (1-402)

Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy         135 AspCysTrpGluProValGlnGlu 142
               |||||||||||||||||||||||
Db         361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 9
AAA03771
ID   AAA03771 standard; DNA; 402 BP.
XX
AC   AAA03771;
XX
DT   19-MAY-2000  (first entry)
XX
DE   Human G-CSF mutant DNA sequence SEQ ID NO:176.
XX
KW   Human; interleukin 3; IL-3; mutant; mutein; CSF; cytokine;
KW   colony stimulating factor; haematopoietic growth factor; lymphokine;
KW   fusion protein; haematopoietic disorder; infection; cancer;
KW   radiation therapy; chemotherapy; bone marrow suppressive drug;
KW   bone marrow activation; blood cell activation; blood transplant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   US6022535-A.
XX
PD   08-FEB-2000.
XX
PF   06-JUN-1995;   95US-00469318.
XX
PR   04-FEB-1994;   94US-00192325.
PR   02-FEB-1995;   95WO-US001185.
PR   06-APR-1995;   95US-00411795.
XX
PA   (SEAR ) SEARLE & CO G D.
XX
PI   Bauer SC,  Abrams MA,  Braford-Goldberg SR,  Easton AM,  Klein BK;
PI   Paik K,  Thomas JW,  Mckearn JP,  Olins PO,  Caparon MH;
XX
DR   WPI; 2000-160368/14.
XX
PT   Treating hematopoietic disorders with fusion proteins comprising mutated
PT   interleukin-3 fused with secondary colony stimulating factors or other
PT   interleukin-3 variants.
XX
PS   Example 19; Col 171-174; 276pp; English.
XX
CC   Methods have been developed for treating haematopoietic disorders with
CC   fusion proteins comprising recombinant, mutated human interleukin-3 (hIL-
CC   3) variants or mutant proteins (muteins) fused with secondary colony
CC   stimulating factors (CSFs) (e.g. cytokines, lymphokines, interleukin
CC   and/or haematopoietic colony stimulating factors) or other interleukin-3
CC   variants with or without a linker. The methods may be used in vivo to
CC   treat haematopoietic disorders resulting from bacterial, viral and fungal
CC   infections, cancer radiation therapy, chemotherapy or bone marrow
CC   suppressive drugs. They may also be used in vitro to stimulate bone
CC   marrow and blood cell activation and growth prior to infusion of the bone
CC   marrow and blood transplants into patients. IL-3 is a haematopoietic
CC   growth factor which has the property of being able to promote the
CC   survival, growth and differentiation of haematopoietic cells. The fusion
CC   molecules are characterised by possessing the usual activity of both of
CC   their constituent peptides and further by having a biological or
CC   physiological activity greater than the additive function of the IL-3 or
CC   second CSF alone (i.e. the peptides act synergistically). Their activity
CC   may also be further enhanced by the mutations they comprise. The
CC   variations may further reduce undesirable side effects associated with IL
CC   -3. AAY53130 to AAY53226, and AAA03721 to AAA03782 represent sequences
CC   used in the exemplification of the present invention
XX
SQ   Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.59e-67        Length:         402
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     3               Gaps:           0

US-10-723-083-2 (1-142) x AAA03771 (1-402)

Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy         135 AspCysTrpGluProValGlnGlu 142
               |||||||||||||||||||||||
Db         361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 10
ABX00086
ID   ABX00086 standard; DNA; 402 BP.
XX
AC   ABX00086;
XX
DT   18-DEC-2002  (first entry)
XX
DE   Human interleukin-3 associated DNA sequence #77.
XX
KW   Haematopoietic factor; GM-CSF; colony stimulating factor; CSF-1; ds;
```

KW G-CSF; G-CSFSer17; c-mpl ligand; TPO; MGDF; erythropoietin; flt3 ligand;
KW human growth hormone; B-cell growth factor; leukaemia;
KW B-cell differentiation factor; eosinophil differentiation factor;
KW stem cell factor; SCF; cyclic neutropenia; aplastic anaemia;
KW thrombocytopenia; idiopathic neutropenia; Chediak-Higashi syndrome;
KW systemic lupus erythematosus; SLE; myelodysplastic syndrome;
KW myelofibrosis; Interleukin-3; IL-3; stem cell.
XX
OS Unidentified.
XX
PN US6436387-B1.
XX
PD 20-AUG-2002.
XX
PF 09-DEC-1996; 96US-00762227.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 04-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 2002-749206/81.
XX
PT Ex vivo expansion of stem cells, for enhancing transduction efficiency of
PT cultured stem cells, comprises culturing stem cells in growth medium
PT having mutant interleukin-3, and hematopoietic factor, and harvesting
PT cultured cells.
XX
PS Disclosure; Col 299-300; 203pp; English.
XX
CC The invention relates to ex vivo expansion of stem cells, comprises
CC culturing stem cells with a growth medium comprising a chimaera protein,
CC and harvesting the cultured stem cells. The chimaera is based on a
CC mutated human interleukin-3 (IL_3) sequence coupled to a haematopoietic
CC factor (e.g. GM-CSF (colony stimulating factor), CSF-1, G-CSF, G-
CC CSFSer17, c-mpl ligand TPO, MGDF, erythropoietin, IL-1-13, IL-15, IL-16,
CC flt3 ligand, human growth hormone, B-cell growth factor, B-cell
CC differentiation factor, eosinophil differentiation factor and stem cell
CC factor (SCF)) via a peptide linker. The formula for the chimaera is given
CC in the specification. Also included is a method for enhancing the
CC efficiency of the transduction of cultured stem cells by a heterologous
CC gene, comprising: (a) removing stem cells from a patient or donor; (b)
CC culturing the stem cells with a growth medium comprising the chimaera (c)
CC transducing DNA into cultured cells; and (d) harvesting the transduced
CC cells. The method is useful for ex vivo expansion of stem cells, and
CC enhancing the efficiency of the transduction of cultured stem cells by a
CC heterologous gene. The method is also useful for treating a patient
CC having a haematopoietic disorder. The expanded haematopoietic cells are
CC also useful in the treatment of cyclic neutropenia, aplastic anaemia,
CC thrombocytopenia, idiopathic neutropenia, Chediak-Higashi syndrome,
CC systemic lupus erythematosus (SLE), leukaemia, myelodysplastic syndrome
CC and myelofibrosis. The present sequence is an IL-3 mutant associated DNA
CC sequence. Note: The present sequence is included in the sequence listing
CC but is not mentioned anywhere else in the specification
XX
SQ Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.59e-67	Length:	402
Score:	678.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.63%	Indels:	0
DB:	6	Gaps:	0

US-10-723-083-2 (1-142) x ABX00086 (1-402)

```
Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384
```

RESULT 11
ADJ14388
ID ADJ14388 standard; DNA; 402 BP.
XX
AC ADJ14388;
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA related to human interleukin-3 (IL-3) mutant protein - SEQ ID 151.
XX
KW stem cell; antianaemic; immunostimulant; immunomodulator;
KW antiinflammatory; dermatological; immunosuppressive; cytostatic;
KW neuroprotective; haemopoietic disorder; gene therapy; myeloid; erythroid;
KW lymphoid; megakaryocyte; aplastic anaemia; periodic neutropenia;
KW Chediak-Higashi syndrome; systemic lupus erythematosus; leukaemia;
KW myelodysplastic syndrome; myelofibrosis; interleukin-3; IL-3; ds.
XX
OS Unidentified.
XX
PN US2003185790-A1.
XX
PD 02-OCT-2003.
XX
PF 26-FEB-2002; 2002US-00083446.
XX
PR 24-NOV-1992; 92US-00981044.
PR 22-NOV-1993; 93WO-US011197.
PR 04-FEB-1994; 94US-00192325.
PR 02-FEB-1995; 95WO-US001185.
PR 06-APR-1995; 95US-00411795.
PR 06-JUN-1995; 95US-00446872.
PR 09-DEC-1996; 96US-00762227.
XX
PA (BAUE/) BAUER S C.
PA (ABRA/) ABRAMS M A.
PA (BRAF/) BRAFORD-GOLDBERG S R.
PA (CAPA/) CAPARON M H.
PA (EAST/) EASTON A M.
PA (KLEI/) KLEIN B K.
PA (MCKE/) MCKEARN J P.
PA (OLIN/) OLINS P O.
PA (PAIK/) PAIK K.
PA (THOM/) THOMAS J W.
XX

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PI   Bauer SC, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI   Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR   WPI; 2004-096775/10.
XX
PT   Ex vivo expansion of stem cells, e.g. hematopoietic cells for treating
PT   aplastic anemia, involves culturing the stem cells with growth medium
PT   comprising chimera protein, and harvesting the cultured stem cells.
XX
PS   Disclosure; SEQ ID NO 176; 202pp; English.
XX
CC   The invention relates to a novel method whereby stem cells are ex vivo
CC   expanded via culturing the stem cells with a growth medium comprising a
CC   chimera protein, followed by harvesting of the cultured stem cells. The
CC   method of the invention has antianaemic, immunostimulant,
CC   immunomodulator, antiinflammatory, dermatological, immunosuppressive,
CC   cytostatic and neuroprotective applications and may be useful to target
CC   haemopoietic cells for gene therapy, preferably for treating patients
CC   having a haemopoietic disorder characterised by decreased levels of
CC   myeloid, erythroid, lymphoid, and/or megakaryocyte cells of haemopoietic
CC   system. The expanded ex vivo cells may be used to treat neutropenia,
CC   aplastic anaemia, periodic neutropenia, Chediak-Higashi syndrome,
CC   systemic lupus erythematosus, leukaemia, myelodysplastic syndrome or
CC   myelofibrosis. The current sequence is that of a DNA related to the human
CC   interleukin-3 (IL-3) mutant protein of the invention.
XX
SQ   Sequence 402 BP; 99 A; 124 C; 101 G; 78 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.59e-67      Length:          402
Score:                    678.00        Matches:         128
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              88.63%        Indels:          0
DB:                       12            Gaps:            0

US-10-723-083-2 (1-142) x ADJ14388 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 12
AAN81322
ID   AAN81322 standard; DNA; 410 BP.
XX
AC   AAN81322;
XX
DT   25-MAR-2003  (revised)
DT   06-JAN-1991  (first entry)
XX
DE   Sequence (I) encoding human granulocyte macrophage colony stimulating
DE   factor (hGMCSF) with Ile at 101.
XX
KW   Leukopoenia therapy; bone marrow transplant; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   misc_feature    complement(1. .4)
FT                   /*tag= a
FT                   /note= "Sticky end"
FT   misc_feature    complement(407. .410)
FT                   /*tag= b
FT                   /note= "Sticky end"
XX
PN   JP63269983-A.
XX
PD   08-NOV-1988.
XX
PF   28-APR-1987;   87JP-00106148.
XX
PR   28-APR-1987;   87JP-00106148.
XX
PA   (AMGE-) AMGEN.
PA   (KIRI ) KIRIN BREWERY KK.
XX
DR   WPI; 1988-358227/50.
XX
PT   Human granulocyte macrophage colony stimulus factor prepn. - by forming
PT   plasmid contg. genetic information and Escherichia coli with the plasmid.
XX
PS   Disclosure; Fig 7(1), Page 488; 17pp; Japanese.
XX
CC   An expression plasmid contg. the DNA is prepd. and used to transform
CC   E.coli. The transformant is cultured and hGMCSF is produced into the
CC   medium. hGMCSF stimulates the granulocyte macrophage system stem cell and
CC   promotes the formation of the granulocyte macrophage. hGMCSF is used in
CC   curing leukopoenia caused by radiation therapy, or chemical therapy, or
CC   in promptly propagating leukocytes after bone marrow transplantation.
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 410 BP; 109 A; 106 C; 91 G; 104 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.64e-67      Length:          410
Score:                    678.00        Matches:         128
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              88.63%        Indels:          0
DB:                       1             Gaps:            0

US-10-723-083-2 (1-142) x AAN81322 (1-410)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         11 ATGGCACCAGCTCGATCACCGTCCCCGTCCACTCAACCATGGGAACATGTTAACGCAATC 70

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         71 CAGGAAGCTCGTCGTCTGCTGAACCTGTCTCGTGATACTGCTGCTGAAATGAACGAAACT 130

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        131 GTTGAAGTGATCAGCGAAATGTTCGATCTGCAGGAACCGACTTGTCTGCAAACCCGTCTG 190

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        191 GAACTGTACAAACAAGGTCTGCGTGGTTCTCTGACTAAACTGAAAGGTCCGCTGACTATG 250

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db        251 ATGGCTAGCCATTACAAACAGCATTGTCCGCCGACTCCGGAAACTTCTTGTGCTACTCAG 310

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 ATCATCACTTTCGAATCTTTCAAAGAAAACCTGAAAGATTTCCTGCTGGTTATCCCGTTC 370

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        371 GATTGTTGGGAACCGGTTCAGGAA 394

RESULT 13
AAN90383
ID   AAN90383 standard; DNA; 415 BP.
XX
AC   AAN90383;
XX
DT   25-MAR-2003  (revised)
DT   01-NOV-1989  (first entry)
XX
DE   Synthetic gene for human granulocyte colony stimulating factor.
XX
KW   DNA; BspMI; restriction sites; blunt ends; fusion proteins;
KW   synthetic gene; human granulocyte colony stimulating factor.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             14. .397
FT                   /*tag=  a
XX
PN   GB2212160-A.
XX
PD   19-JUL-1989.
XX
PF   13-NOV-1987;   87GB-00726581.
XX
PR   13-NOV-1987;   87GB-00026581.
XX
PA   (BRBI-) BRITISH BIO-TECHN L.
XX
PI   Edwards RM;
XX
DR   WPI; 1989-208959/29.
DR   P-PSDB; AAP90118.
XX
PT   DNA including recognition site for BspMI enzyme - allowing generation of
PT   blunt end for fusion in prodn. of fusion proteins.
XX
PS   Disclosure; Fig 2; 23pp; English.
XX
CC   Synthetic gene for human granulocyte colony stimulating factor (GM-CSF)
CC   contg. useful restriction sites, and a BspMI site. See corresp. AAP90118.
CC   Useful for generating blunt ends in fusion protein prodn. (Updated on 25-
CC   MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PR
CC   field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 415 BP; 104 A; 130 C; 104 G; 77 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              1.67e-67        Length:         415
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     1               Gaps:           0

US-10-723-083-2 (1-142) x AAN90383 (1-415)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATGGCACCCGCCCGGTCACCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATC 73

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 133

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 193

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 253

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 313

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 373

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        374 GACTGCTGGGAGCCAGTCCAGGAG 397

RESULT 14
AAN90274
ID   AAN90274 standard; DNA; 415 BP.
XX
AC   AAN90274;
XX
DT   25-MAR-2003  (revised)
DT   01-NOV-1989  (first entry)
XX
DE   Synthetic human granulocyte colony stimulating factor.
XX
KW   Synthetic DNA; human granulocyte colony stimulating factor;
KW   restriction sites; cassette mutagenesis; expression system.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             14. .397
FT                   /*tag=  a
XX
PN   GB2212159-A.
XX
PD   19-JUL-1989.
XX
PF   13-NOV-1987;   87GB-00026580.
XX
PR   13-NOV-1987;   87GB-00026580.
XX
PA   (BRBI-) BRITISH BIO-TECHN L.
XX
PI   Edwards RM;
XX
DR   WPI; 1989-208958/29.
DR   P-PSDB; AAP90115.
XX
PT   Human granulocyte-macrophage colony stimulating factor - synthetic DNA
PT   includes restriction sites for cassette mutagenesis and incorporation in
PT   expression systems.
XX
PS   Claim 2; Page 14 and fig 3a; 21pp; English.
XX
CC   Synthetic DNA encoding human granulocyte colony stimulating factor (GM-
CC   CSF), see corresp. AAP90115. Has useful restriction sites for: HindIII;
CC   BspMI; NcoI; BstEII; BsmI; EcoRV; BglI; ApaI; BalI; XmnI; BamHI; and
CC   EcoRI. Used to facilitate cassette mutagenesis of selected regions.
CC   Synthesised by phosphoramidite chemistry, by dividing desired gene into
CC   18 oligomers. (Updated on 25-MAR-2003 to correct PA field.)
XX
```

SQ Sequence 415 BP; 104 A; 130 C; 104 G; 77 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.67e-67	Length:	415
Score:	678.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.63%	Indels:	0
DB:	1	Gaps:	0

US-10-723-083-2 (1-142) x AAN90274 (1-415)

```
Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATGGCACCCGCCCGGTCACCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATC 73

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 133

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 193

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 253

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 313

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 373

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        374 GACTGCTGGGAGCCAGTCCAGGAG 397
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RESULT 15
AAQ97183
ID AAQ97183 standard; DNA; 822 BP.
XX
AC AAQ97183;
XX
DT 25-AUG-1999 (first entry)
XX
DE pMON13035 DNA encoding IL-3 fusion protein.
XX
KW Interleukin; hIL-3; CSF; colony stimulating factor; cytokine; lymphokine;
KW mutant; mutein; fusion protein; linker; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9521254-A1.
XX
PD 10-AUG-1995.
XX
PF 02-FEB-1995; 95WO-US001185.
XX
PR 04-FEB-1994; 94US-00192325.
XX
PA (SEAR) SEARLE & CO G D.
XX
PI Bauer CS, Abrams MA, Braford-Goldberg SR, Caparon MH, Easton AM;
PI Klein BK, Mckearn JP, Olins PO, Paik K, Thomas JW;
XX
DR WPI; 1995-283774/37.
DR P-PSDB; AAR79320.
XX
PT Fusion proteins comprising a human interleukin-3 variant, a linker and
PT interleukin-3, a variant or a colony stimulating factor - useful to
PT increase haematopoietic cell prodn. in a mammal.
XX
PS Claim 22; Page 167-168; 447pp; English.
XX
CC A new fusion protein is disclosed which has the formula R1-L-R2, R2-L-R1,
CC R1-R2, R2-R1, R1-L-R1 or R1-R1, where R1 is a mutant or variant of human
CC interleukin-3 (hIL-3), R2 is a second colony stimulating factor (CSF)
CC including cytokine, lymphokine, interleukin, haematopoietic growth factor
CC or IL-3 variant, and L is a linker. Generic sequences are described in
CC AAW03235 - AAW03242, and specifically claimed examples are shown in
CC AAR79298-R79335 and AAR79342-R79345. The fusion protein is made by
CC recombinant DNA techniques. Specifically claimed examples of DNA
CC sequences (including the present sequence) which encode these proteins
CC are shown in AAQ97167-Q97204 and AAQ97222-Q97227. The fusion protein is
CC used to increase haematopoietic cell production. It is also useful as an
CC IL-3 antagonist or as a discrete antigenic fragment for production of
CC antibodies useful in immunoassays and immunotherapy. Antagonists are used
CC to block the growth of certain cancer cells and in treatment of asthma.
CC The fusion protein can also be used to stimulate bone marrow and blood
CC cell activation and growth in vitro before infusion; and to treat
CC diseases characterised by decreased levels of myeloid, erythroid,
CC lymphoid and/or megakaryocyte cells of the haematopoietic system. The
CC protein has the usual activity of both its component proteins, but may
CC have increased synergistic activity and reduced undesired side effects
XX
SQ Sequence 822 BP; 222 A; 244 C; 180 G; 176 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	4.25e-67	Length:	822
Score:	678.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.63%	Indels:	0
DB:	2	Gaps:	0

US-10-723-083-2 (1-142) x AAQ97183 (1-822)

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Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
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Db        439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 498

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 558

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 618

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 678

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 798

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        799 GACTGCTGGGAGCCAGTCCAGGAG 822
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Search completed: March 11, 2005, 18:36:51
Job time : 480 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2005, 17:26:51 ; Search time 3628 Seconds
(without alignments)
1896.538 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHHHSSGIEGRMAPARS.....ENLKDFLLVIPFDCWEPVQE 142

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_htg:*
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13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	682	89.2	777	6	AR202206	AR202206 Sequence
2	682	89.2	777	6	AR223208	AR223208 Sequence
3	678	88.6	384	6	E11629	E11629 hGM-CSF-enc
4	678	88.6	402	6	AR202280	AR202280 Sequence
5	678	88.6	402	6	AR223282	AR223282 Sequence
6	678	88.6	415	6	A00367	A00367 Artificial
c 7	678	88.6	415	6	A00368	A00368 Artificial
8	678	88.6	415	6	A14305	A14305 GM-CSF gene
c 9	678	88.6	415	6	A14306	A14306 GM-CSF gene
10	678	88.6	822	6	AR202220	AR202220 Sequence
11	678	88.6	822	6	AR223222	AR223222 Sequence
12	678	88.6	903	6	AR202217	AR202217 Sequence
13	678	88.6	903	6	AR223219	AR223219 Sequence
14	676	88.4	1630	6	BD222938	BD222938 Heteromin
15	676	88.4	1630	6	AX023365	AX023365 Sequence
16	673	88.0	384	6	A20082	A20082 PstI-Hind I
17	673	88.0	384	6	E11628	E11628 hGM-CSF-enc
c 18	673	88.0	392	6	A20083	A20083 PstI-Hind I
19	673	88.0	392	6	I49837	I49837 Sequence 1
20	673	88.0	418	6	A11762	A11762 Artificial
c 21	673	88.0	418	6	A11763	A11763 Artificial
22	673	88.0	435	6	CQ834914	CQ834914 Sequence
23	673	88.0	435	6	CQ834915	CQ834915 Sequence
24	673	88.0	435	6	AR533388	AR533388 Sequence
25	673	88.0	435	6	BD105958	BD105958 Animal mo
26	673	88.0	436	6	E01740	E01740 gene encodi
27	673	88.0	505	6	I08646	I08646 Sequence 3
28	673	88.0	505	9	HUMCSFGMB	M11734 Human granu
29	673	88.0	644	6	E01141	E01141 cDNA encodi
30	673	88.0	660	6	AR364645	AR364645 Sequence
31	673	88.0	661	6	E00951	E00951 cDNA encodi
32	673	88.0	661	6	I04859	I04859 Sequence 3
33	673	88.0	661	6	AR363793	AR363793 Sequence
34	673	88.0	756	6	CQ721607	CQ721607 Sequence
35	673	88.0	756	6	CQ803372	CQ803372 Sequence
36	673	88.0	763	6	E02287	E02287 DNA encodin
37	673	88.0	787	6	I08093	I08093 Sequence 1
38	673	88.0	787	6	I08094	I08094 Sequence 1
39	673	88.0	787	6	I08401	I08401 Sequence 1
40	673	88.0	787	6	I09140	I09140 Sequence 1
41	673	88.0	787	6	I09160	I09160 Sequence 21
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43	673	88.0	896	6	A20086	A20086 BamHI-HindI
c 44	673	88.0	896	6	A20087	A20087 BamHI-HindI
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ALIGNMENTS

RESULT 1
AR202206
LOCUS AR202206 777 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 55 from patent US 6361977.
ACCESSION AR202206
VERSION AR202206.1 GI:20256745
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 777)
AUTHORS Bauer,S.Christopher., Abrams,M.Allen., Braford-Goldberg,S.Ruth., Caparon,M.Helena., Easton,A.Michael., Klein,B.Kure., McKearn,J.P., Olins,P.O., Paik,K. and Thomas,J.W.
TITLE Methods of using multivariant IL-3 hematopoiesis fusion protein
JOURNAL Patent: US 6361977-A 55 26-MAR-2002;
FEATURES Location/Qualifiers
source 1. .777
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

Pred. No.:	9.49e-60	Length:	777
Score:	682.00	Matches:	130
Percent Similarity:	97.01%	Conservative:	0
Best Local Similarity:	97.01%	Mismatches:	4
Query Match:	89.15%	Indels:	0

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DB:                    6              Gaps:          0

US-10-723-083-2 (1-142) x AR202206 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
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Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
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Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
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Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
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Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 2
AR223208
LOCUS       AR223208                 777 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 55 from patent US 6436387.
ACCESSION   AR223208
VERSION     AR223208.1  GI:23331216
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 777)
  AUTHORS   Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
            Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P.O., Paik,K. and
            Thomas,J.W.
  TITLE     Methods of ex-vivo expansion of hematopoietic cells using
            multivariant IL-3 hematopoiesis chimera proteins
  JOURNAL   Patent: US 6436387-A 55 20-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .777
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              9.49e-60        Length:         777
Score:                  682.00          Matches:        130
Percent Similarity:     97.01%          Conservative:   0
Best Local Similarity:  97.01%          Mismatches:     4
Query Match:            89.15%          Indels:         0
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x AR223208 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||                ||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
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Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
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Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 3
E11629
LOCUS       E11629                   384 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  hGM-CSF-encoding DNA for efficient expression in E.coli.
ACCESSION   E11629
VERSION     E11629.1  GI:22025265
KEYWORDS    JP 1996173185-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Matsuki,S., Ozawa,T. and Tamai,Y.
  TITLE     PRODUCTION OF STIMULATING FACTOR FOR HUMAN GRANULOCYTIC MACROPHAGE
            COLONY
  JOURNAL   Patent: JP 1996173185-A 2 09-JUL-1996;
            AMGEN, KIRIN BREWERY CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1996173185-A/2
            PD   09-JUL-1996
            PF   28-APR-1987 JP 1995263370
            PI   MATSUKI SHIGERU, OZAWA TADASHI, TAMAI YUKIO
            PC   C12P21/02,C12N1/21,C12N15/09,(C12P21/02,C12R1:19),(C12N1/21,
            PC   C12R1:19);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .384
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .384
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

Alignment Scores:
Pred. No.:              1.06e-59        Length:         384
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x E11629 (1-384)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
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Db          1 ATGGCACCAGCTCGATCACCGTCCCCGTCCACTCAACCATGGGAACATGTTAACGCAATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 CAGGAAGCTCGTCGTCTGCTGAACCTGTCTCGTGATACTGCTGCTGAAATGAACGAAACT 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTTGAAGTGATCAGCGAAATGTTCGATCTGCAGGAACCGACTTGTCTGCAAACCCGTCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAACTGTACAAACAAGGTCTGCGTGGTTCTCTGACTAAACTGAAAGGTCCGCTGACTATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
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Db        241 ATGGCTAGCCATTACAAACAGCATTGTCCGCCGACTCCGGAAACTTCTTGTGCTACTCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
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Db        301 ATCATCACTTTCGAATCTTTCAAAGAAAACCTGAAAGATTTCCTGCTGGTTATCCCGTTC 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GATTGTTGGGAACCGGTTCAGGAA 384

RESULT 4
AR202280
LOCUS       AR202280                402 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 176 from patent US 6361977.
ACCESSION   AR202280
VERSION     AR202280.1  GI:20256819
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Bauer,S.Christopher., Abrams,M.Allen., Braford-Goldberg,S.Ruth.,
            Caparon,M.Helena., Easton,A.Michael., Klein,B.Kure., McKearn,J.P.,
            Olins,P.O., Paik,K. and Thomas,J.W.
  TITLE     Methods of using multivariant IL-3 hematopoiesis fusion protein
  JOURNAL   Patent: US 6361977-A 176 26-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .402
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ORIGIN

Alignment Scores:
Pred. No.:              1.12e-59        Length:         402
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
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US-10-723-083-2 (1-142) x AR202280 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
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Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
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Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 5
AR223282
LOCUS       AR223282                402 bp    DNA     linear   PAT 26-SEP-2002
DEFINITION  Sequence 176 from patent US 6436387.
ACCESSION   AR223282
VERSION     AR223282.1  GI:23331290
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
            Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P.O., Paik,K. and
            Thomas,J.W.
  TITLE     Methods of ex-vivo expansion of hematopoietic cells using
            multivariant IL-3 hematopoiesis chimera proteins
  JOURNAL   Patent: US 6436387-A 176 20-AUG-2002;
FEATURES             Location/Qualifiers
     source          1. .402
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              1.12e-59        Length:         402
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x AR223282 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 6
A00367
LOCUS       A00367                  415 bp    DNA     linear   PAT 09-MAR-1993
```

```
DEFINITION  Artificial gene for granulocyte/macrophage colony stimulating
            factor.
ACCESSION   A00367
VERSION     A00367.1  GI:344179
KEYWORDS    granulocyte-macrophage colony stimulating factor; synthetic gene.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   .
  TITLE     Synthetic-gene
  JOURNAL   Patent: GB 2212159-A 2 19-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             14. .400
                     /note="synthetic"
                     /codon_start=1
                     /transl_table=11
                     /product="granulocyte/macrophage colony stimulating
                     factor"
                     /protein_id="CAA00057.1"
                     /db_xref="GI:344180"
                     /translation="MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVI
                     SEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQII
                     TFESFKENLKDFLLVIPFDCWEPVQE"
ORIGIN

Alignment Scores:
Pred. No.:                1.16e-59       Length:          415
Score:                    678.00         Matches:         128
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              88.63%         Indels:          0
DB:                       6              Gaps:            0

US-10-723-083-2 (1-142) x A00367 (1-415)

Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          14 ATGGCACCCGCCCGGTCACCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATC 73

Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          74 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 133

Qy          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         134 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 193

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         194 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 253

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         254 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 313

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         314 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 373

Qy         135 AspCysTrpGluProValGlnGlu 142
               |||||||||||||||||||||||
Db         374 GACTGCTGGGAGCCAGTCCAGGAG 397

RESULT 7
A00368/c
LOCUS       A00368                   415 bp    DNA     linear   PAT 09-MAR-1993
DEFINITION  Artificial gene for granulocyte/macrophage colony stimulating
            factor, reverse complement.
ACCESSION   A00368
VERSION     A00368.1  GI:344181
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   .
  TITLE     Synthetic-gene
  JOURNAL   Patent: GB 2212159-A 3 19-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:                1.16e-59       Length:          415
Score:                    678.00         Matches:         128
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              88.63%         Indels:          0
DB:                       6              Gaps:            0

US-10-723-083-2 (1-142) x A00368 (1-415)

Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         402 ATGGCACCCGCCCGGTCACCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATC 343

Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         342 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 283

Qy          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         282 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 223

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         222 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 163

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         162 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 103

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         102 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 43

Qy         135 AspCysTrpGluProValGlnGlu 142
               |||||||||||||||||||||||
Db          42 GACTGCTGGGAGCCAGTCCAGGAG 19

RESULT 8
A14305
LOCUS       A14305                   415 bp    DNA     linear   PAT 18-JAN-1994
DEFINITION  GM-CSF gene (from Homo sapiens).
ACCESSION   A14305
VERSION     A14305.1  GI:491775
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   .
  TITLE     DNA sequence
  JOURNAL   Patent: GB 2212160-A 2 19-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                /db_xref="taxon:32630"
     gene       14. .400
                /gene="human GM-CSF gene"
     CDS        14. .400
                /gene="human GM-CSF gene"
                /codon_start=1
                /transl_table=11
                /protein_id="CAA01150.1"
                /db_xref="GI:491776"
                /translation="MAPARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVI
                SEMFDLQEPTCLQTRLELYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQII
                TFESFKENLKDFLLVIPFDCWEPVQE"
ORIGIN

Alignment Scores:
Pred. No.:              1.16e-59        Length:         415
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x A14305 (1-415)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         14 ATGGCACCCGCCCGGTCACCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATC 73

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         74 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 133

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        134 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 193

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        194 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 253

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        254 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 313

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        314 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 373

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        374 GACTGCTGGGAGCCAGTCCAGGAG 397

RESULT 9
A14306/c
LOCUS       A14306                  415 bp    DNA     linear   PAT 18-JAN-1994
DEFINITION  GM-CSF gene (from Homo sapiens).
ACCESSION   A14306
VERSION     A14306.1  GI:489685
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 415)
  AUTHORS   .
  TITLE     DNA sequence
  JOURNAL   Patent: GB 2212160-A 3 19-JUL-1989;
FEATURES             Location/Qualifiers
     source          1. .415
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

Alignment Scores:
Pred. No.:              1.16e-59        Length:         415
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x A14306 (1-415)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        402 ATGGCACCCGCCCGGTCACCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATC 343

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        342 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 283

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        282 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 223

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        222 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 163

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        162 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 103

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 43

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db         42 GACTGCTGGGAGCCAGTCCAGGAG 19

RESULT 10
AR202220
LOCUS       AR202220                822 bp    DNA     linear   PAT 20-APR-2002
DEFINITION  Sequence 69 from patent US 6361977.
ACCESSION   AR202220
VERSION     AR202220.1  GI:20256759
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 822)
  AUTHORS   Bauer,S.Christopher., Abrams,M.Allen., Braford-Goldberg,S.Ruth.,
            Caparon,M.Helena., Easton,A.Michael., Klein,B.Kure., McKearn,J.P.,
            Olins,P.O., Paik,K. and Thomas,J.W.
  TITLE     Methods of using multivariant IL-3 hematopoiesis fusion protein
  JOURNAL   Patent: US 6361977-A 69 26-MAR-2002;
FEATURES             Location/Qualifiers
     source          1. .822
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

Alignment Scores:
Pred. No.:              2.58e-59        Length:         822
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x AR202220 (1-822)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 498
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Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         499 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 558

Qy          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 618

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         619 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 678

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 798

Qy         135 AspCysTrpGluProValGlnGlu 142
               |||||||||||||||||||||||
Db         799 GACTGCTGGGAGCCAGTCCAGGAG 822
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RESULT 11
AR223222
LOCUS AR223222 822 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 69 from patent US 6436387.
ACCESSION AR223222
VERSION AR223222.1 GI:23331230
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 822)
AUTHORS Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H., Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P.O., Paik,K. and Thomas,J.W.
TITLE Methods of ex-vivo expansion of hematopoietic cells using multivariant IL-3 hematopoiesis chimera proteins
JOURNAL Patent: US 6436387-A 69 20-AUG-2002;
FEATURES Location/Qualifiers
source 1. .822
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.58e-59	Length:	822
Score:	678.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.63%	Indels:	0
DB:	6	Gaps:	0

US-10-723-083-2 (1-142) x AR223222 (1-822)

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Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 498

Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         499 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 558

Qy          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 618

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         619 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 678

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 798

Qy         135 AspCysTrpGluProValGlnGlu 142
               |||||||||||||||||||||||
Db         799 GACTGCTGGGAGCCAGTCCAGGAG 822
```

RESULT 12
AR202217
LOCUS AR202217 903 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 66 from patent US 6361977.
ACCESSION AR202217
VERSION AR202217.1 GI:20256756
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 903)
AUTHORS Bauer,S.Christopher., Abrams,M.Allen., Braford-Goldberg,S.Ruth., Caparon,M.Helena., Easton,A.Michael., Klein,B.Kure., McKearn,J.P., Olins,P.O., Paik,K. and Thomas,J.W.
TITLE Methods of using multivariant IL-3 hematopoiesis fusion protein
JOURNAL Patent: US 6361977-A 66 26-MAR-2002;
FEATURES Location/Qualifiers
source 1. .903
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Alignment Scores:

Pred. No.:	2.87e-59	Length:	903
Score:	678.00	Matches:	128
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	88.63%	Indels:	0
DB:	6	Gaps:	0

US-10-723-083-2 (1-142) x AR202217 (1-903)

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Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
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Db         520 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 579

Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
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Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
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Db         760 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 819

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
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Db         820 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 879

Qy         135 AspCysTrpGluProValGlnGlu 142
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Db         880 GACTGCTGGGAGCCAGTCCAGGAG 903
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DEFINITION  Sequence 66 from patent US 6436387.
ACCESSION   AR223219
VERSION     AR223219.1  GI:23331227
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   Bauer,S.C., Abrams,M.A., Braford-Goldberg,S.R., Caparon,M.H.,
            Easton,A.M., Klein,B.K., McKearn,J.P., Olins,P.O., Paik,K. and
            Thomas,J.W.
  TITLE     Methods of ex-vivo expansion of hematopoietic cells using
            multivariant IL-3 hematopoiesis chimera proteins
  JOURNAL   Patent: US 6436387-A 66 20-AUG-2002;
FEATURES             Location/Qualifiers
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ORIGIN

Alignment Scores:
Pred. No.:              2.87e-59        Length:         903
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
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US-10-723-083-2 (1-142) x AR223219 (1-903)

Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
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Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
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Db         640 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 699

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
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Db         700 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 759

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
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Db         760 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 819

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         820 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 879

Qy         135 AspCysTrpGluProValGlnGlu 142
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Db         880 GACTGCTGGGAGCCAGTCCAGGAG 903

RESULT 14
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LOCUS       BD222938               1630 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Heterominibodies.
ACCESSION   BD222938
VERSION     BD222938.1  GI:33032708
KEYWORDS    JP 2002521053-A/32.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
  TITLE     Heterominibodies
  JOURNAL   Patent: JP 2002521053-A 32 16-JUL-2002;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            OS   Mus musculus (mouse)
            PN   JP 2002521053-A/32
            PD   16-JUL-2002
            PF   28-JUL-1999 JP 2000562401
            PR   28-JUL-1998 EP   98114082.5
            PI   PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
            BORSCHERT,
            PI   FLORIAN ZETTL
            PC   C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
            PC   C07K19/00,
            PC   C12N5/10,C12P21/02,G01N33/53,G01N33/53//(C12N5/10,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
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Alignment Scores:
Pred. No.:              9.1e-59         Length:         1630
Score:                  676.00          Matches:        128
Percent Similarity:     98.46%          Conservative:   0
Best Local Similarity:  98.46%          Mismatches:     2
Query Match:            88.37%          Indels:         0
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x BD222938 (1-1630)

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Qy          33 AlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsn 52
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Db        1260 GCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAAT 1319

Qy          53 GluThrValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThr 72
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Qy          73 ArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeu 92
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Db        1380 CGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG 1439

Qy          93 ThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAla 112
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Db        1440 ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCA 1499

Qy         113 ThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIle 132
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Qy         133 ProPheAspCysTrpGluProValGlnGlu 142
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Db        1560 CCCTTTGACTGCTGGGAGCCAGTCCAGGAG 1589

RESULT 15
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LOCUS       AX023365               1630 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 36 from Patent WO0006605.
ACCESSION   AX023365
VERSION     AX023365.1  GI:10183777
KEYWORDS    .
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SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
  TITLE     Heterominibodies
  JOURNAL   Patent: WO 0006605-A 36 10-FEB-2000;
            KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
            BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
            BIOMEDIZINIS (DE)
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ORIGIN

Alignment Scores:
Pred. No.:              9.1e-59         Length:         1630
Score:                  676.00          Matches:        128
Percent Similarity:     98.46%          Conservative:   0
Best Local Similarity:  98.46%          Mismatches:     2
Query Match:            88.37%          Indels:         0
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x AX023365 (1-1630)

Qy         13 GlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsn 32
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Qy         33 AlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsn 52
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Db       1260 GCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAAT 1319

Qy         53 GluThrValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThr 72
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1320 GAAACAGTAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACC 1379

Qy         73 ArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeu 92
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1380 CGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTG 1439

Qy         93 ThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAla 112
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1440 ACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCA 1499

Qy        113 ThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIle 132
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Db       1500 ACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATC 1559

Qy        133 ProPheAspCysTrpGluProValGlnGlu 142
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Db       1560 CCCTTTGACTGCTGGGAGCCAGTCCAGGAG 1589


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Job time : 3634 secs

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Searched: 1202784 seqs, 818138359 residues

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Minimum DB seq length: 0
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SUMMARIES

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2	682	89.2	777	3	US-08-468-609A-55	Sequence 55, Appl
3	682	89.2	777	3	US-08-446-872A-55	Sequence 55, Appl
4	682	89.2	777	3	US-08-762-227A-55	Sequence 55, Appl
5	682	89.2	777	5	PCT-US95-01185-55	Sequence 55, Appl
6	678	88.6	402	3	US-08-469-318-176	Sequence 176, App
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8	678	88.6	402	3	US-08-446-872A-176	Sequence 176, App
9	678	88.6	402	3	US-08-762-227A-176	Sequence 176, App
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13	678	88.6	822	3	US-08-446-872A-69	Sequence 69, Appl
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18	678	88.6	903	3	US-08-446-872A-66	Sequence 66, Appl
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22	673	88.0	435	3	US-08-848-760B-8	Sequence 8, Appli
23	673	88.0	435	4	US-09-826-025-8	Sequence 8, Appli
24	673	88.0	435	4	US-10-188-056-31	Sequence 31, Appl
25	673	88.0	435	4	US-10-188-056-32	Sequence 32, Appl
26	673	88.0	660	6	5391485-2	Patent No. 5391485
27	673	88.0	660	6	5391485-2	Patent No. 5391485
28	673	88.0	661	6	5229496-1	Patent No. 5229496
29	673	88.0	661	6	5229496-1	Patent No. 5229496
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33	673	88.0	905	6	5200327-3	Patent No. 5200327
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36	673	88.0	1011	4	US-09-976-594-275	Sequence 275, App
37	673	88.0	1318	3	US-09-310-842-3	Sequence 3, Appli
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39	673	88.0	1588	3	US-08-579-823A-1	Sequence 1, Appli
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ALIGNMENTS

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US-08-469-318-55
; Sequence 55, Application US/08469318
; Patent No. 6022535
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;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,318
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/446,872
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  777 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-469-318-55

Alignment Scores:
Pred. No.:                1.89e-76      Length:          777
Score:                    682.00        Matches:         130
Percent Similarity:       97.01%        Conservative:    0
Best Local Similarity:    97.01%        Mismatches:      4
Query Match:              89.15%        Indels:          0
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 2
US-08-468-609A-55
; Sequence 55, Application US/08468609A
; Patent No. 6030812
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,609A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  777 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-468-609A-55

Alignment Scores:
Pred. No.:              1.89e-76        Length:          777
Score:                  682.00          Matches:         130
Percent Similarity:     97.01%          Conservative:    0
Best Local Similarity:  97.01%          Mismatches:      4
Query Match:            89.15%          Indels:          0
DB:                     3               Gaps:            0

US-10-723-083-2 (1-142) x US-08-468-609A-55 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||              ||||||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 3
US-08-446-872A-55
; Sequence 55, Application US/08446872A
; Patent No. 6361977
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis
;    TITLE OF INVENTION:  Fusion Protein
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
```

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;       STATE:  Illinois
;       COUNTRY:  USA
;       ZIP:  60680
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/446,872A
;       FILING DATE:  06-JUN-1995
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/192,325
;       FILING DATE:  14-FEB-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bennett, Dennis A.
;       REGISTRATION NUMBER:  34,547
;       REFERENCE/DOCKET NUMBER:  C-2790/1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (314)737-6986
;       TELEFAX:  (314)737-6972
;   INFORMATION FOR SEQ ID NO:  55:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  777 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
US-08-446-872A-55

Alignment Scores:
Pred. No.:              1.89e-76        Length:         777
Score:                  682.00          Matches:        130
Percent Similarity:     97.01%          Conservative:   0
Best Local Similarity:  97.01%          Mismatches:     4
Query Match:            89.15%          Indels:         0
DB:                     3               Gaps:           0

US-10-723-083-2 (1-142) x US-08-446-872A-55 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||          ||||||||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 4
US-08-762-227A-55
; Sequence 55, Application US/08762227A
; Patent No. 6436387
;   GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
;                  Caparon, Maire H.
;                  Easton, Alan M.
;                  Klein, Barbara K.
;                  McKearn, John P.
;                  Olins, Peter O.
;                  Paik, Kumnan
;                  Thomas, John W.
;       TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
;                           Fusion Protein
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
;                       Corporate Patent Dept.
;            STREET: P. O. Box 5110
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60680
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/762,227A
;            FILING DATE: 09-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/192,325
;            FILING DATE: 14-FEB-1994
;            APPLICATION NUMBER: US 08/446,872
;            FILING DATE: 06-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bennett, Dennis A.
;            REGISTRATION NUMBER: 34,547
;            REFERENCE/DOCKET NUMBER: C-2790/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (708)470-6501
;            TELEFAX: (708)470-6881
;   INFORMATION FOR SEQ ID NO: 55:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 777 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-08-762-227A-55

Alignment Scores:
Pred. No.:              1.89e-76        Length:         777
Score:                  682.00          Matches:        130
Percent Similarity:     97.01%          Conservative:   0
Best Local Similarity:  97.01%          Mismatches:     4
Query Match:            89.15%          Indels:         0
DB:                     3               Gaps:           0

US-10-723-083-2 (1-142) x US-08-762-227A-55 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||          ||||||||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 5
PCT-US95-01185-55
; Sequence 55, Application PC/TUS9501185
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01185
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192325
;      FILING DATE:  14-FEB-1994
;  INFORMATION FOR SEQ ID NO:  55:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  777 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US95-01185-55

Alignment Scores:
Pred. No.:              1.89e-76        Length:         777
Score:                  682.00          Matches:        130
Percent Similarity:     97.01%          Conservative:   0
Best Local Similarity:  97.01%          Mismatches:     4
Query Match:            89.15%          Indels:         0
DB:                     5               Gaps:           0

US-10-723-083-2 (1-142) x PCT-US95-01185-55 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||              ||||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              ||||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 6
US-08-469-318-176
; Sequence 176, Application US/08469318
; Patent No. 6022535
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,318
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/446,872
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  176:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  402 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-469-318-176

Alignment Scores:
Pred. No.:              2.23e-76        Length:         402
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     3               Gaps:           0

US-10-723-083-2 (1-142) x US-08-469-318-176 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
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Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
                ||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 7
US-08-468-609A-176
; Sequence 176, Application US/08468609A
; Patent No. 6030812
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,609A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  176:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  402 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-468-609A-176

Alignment Scores:
Pred. No.:              2.23e-76        Length:         402
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     3               Gaps:           0

US-10-723-083-2 (1-142) x US-08-468-609A-176 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
                ||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 8
US-08-446-872A-176
; Sequence 176, Application US/08446872A
; Patent No. 6361977
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis
;    TITLE OF INVENTION:  Fusion Protein
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,872A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  176:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  402 base pairs
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-446-872A-176

Alignment Scores:
Pred. No.:              2.23e-76        Length:         402
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     3               Gaps:           0

US-10-723-083-2 (1-142) x US-08-446-872A-176 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 9
US-08-762-227A-176
; Sequence 176, Application US/08762227A
; Patent No. 6436387
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Thomas, John W.
;        TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
;                            Fusion Protein
;        NUMBER OF SEQUENCES: 197
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
;                        Corporate Patent Dept.
;             STREET: P. O. Box 5110
;             CITY: Chicago
;             STATE: Illinois
;             COUNTRY: USA
;             ZIP: 60680
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/762,227A
;             FILING DATE: 09-Dec-1996
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bennett, Dennis A.
;             REGISTRATION NUMBER: 34,547
;             REFERENCE/DOCKET NUMBER: C-2790/5
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (708)470-6501
;             TELEFAX: (708)470-6881
;   INFORMATION FOR SEQ ID NO: 176:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 402 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 176:
US-08-762-227A-176

Alignment Scores:
Pred. No.:              2.23e-76        Length:         402
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     3               Gaps:           0

US-10-723-083-2 (1-142) x US-08-762-227A-176 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 10
PCT-US95-01185-176
; Sequence 176, Application PC/TUS9501185
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
```

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;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01185
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192325
;      FILING DATE:  14-FEB-1994
;  INFORMATION FOR SEQ ID NO:  176:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  402 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US95-01185-176

Alignment Scores:
Pred. No.:              2.23e-76      Length:         402
Score:                  678.00        Matches:        128
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            88.63%        Indels:         0
DB:                     5             Gaps:           0

US-10-723-083-2 (1-142) x PCT-US95-01185-176 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 11
US-08-469-318-69
; Sequence 69, Application US/08469318
; Patent No. 6022535
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/469,318
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/446,872
;      FILING DATE:
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  822 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-469-318-69

Alignment Scores:
Pred. No.:              6.6e-76       Length:         822
Score:                  678.00        Matches:        128
Percent Similarity:     100.00%       Conservative:   0
Best Local Similarity:  100.00%       Mismatches:     0
Query Match:            88.63%        Indels:         0
DB:                     3             Gaps:           0

US-10-723-083-2 (1-142) x US-08-469-318-69 (1-822)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 498

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 558

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 618

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 678

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 798

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        799 GACTGCTGGGAGCCAGTCCAGGAG 822

RESULT 12
US-08-468-609A-69
; Sequence 69, Application US/08468609A
; Patent No. 6030812
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
```

```
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/468,609A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  822 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-468-609A-69

Alignment Scores:
Pred. No.:              6.6e-76        Length:         822
Score:                  678.00         Matches:        128
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            88.63%         Indels:         0
DB:                     3              Gaps:           0

US-10-723-083-2 (1-142) x US-08-468-609A-69 (1-822)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 498

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 558

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 618

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 678

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 798

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||||
Db        799 GACTGCTGGGAGCCAGTCCAGGAG 822
```

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RESULT 13
US-08-446-872A-69
; Sequence 69, Application US/08446872A
; Patent No. 6361977
;  GENERAL INFORMATION:
;    APPLICANT:  Abrams, Mark A.
;    APPLICANT:  Bauer, S. C.
;    APPLICANT:  Braford-Goldberg, Sarah R.
;    APPLICANT:  Caparon, Maire H.
;    APPLICANT:  Easton, Alan M.
;    APPLICANT:  Klein, Barbara K.
;    APPLICANT:  McKearn, John P.
;    APPLICANT:  Olins, Peter O.
;    APPLICANT:  Paik, Kumnan
;    APPLICANT:  Thomas, John W.
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis
;    TITLE OF INVENTION:  Fusion Protein
;    NUMBER OF SEQUENCES:  197
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Dennis A. Bennett, G.D. Searle & Co.,
;      ADDRESSEE:  Corporate Patent Dept.
;      STREET:  P. O. Box 5110
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60680
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/446,872A
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192,325
;      FILING DATE:  14-FEB-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bennett, Dennis A.
;      REGISTRATION NUMBER:  34,547
;      REFERENCE/DOCKET NUMBER:  C-2790/1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (314)737-6986
;      TELEFAX:  (314)737-6972
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  822 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-446-872A-69

Alignment Scores:
Pred. No.:              6.6e-76        Length:         822
Score:                  678.00         Matches:        128
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            88.63%         Indels:         0
DB:                     3              Gaps:           0

US-10-723-083-2 (1-142) x US-08-446-872A-69 (1-822)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
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Db        439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 498

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
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Db        499 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 558

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
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Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet  94
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Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
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Db        679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
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Qy        135 AspCysTrpGluProValGlnGlu 142
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Db        799 GACTGCTGGGAGCCAGTCCAGGAG 822

RESULT 14
US-08-762-227A-69
; Sequence 69, Application US/08762227A
; Patent No. 6436387
;  GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
;                  Caparon, Maire H.
;                  Easton, Alan M.
;                  Klein, Barbara K.
;                  McKearn, John P.
;                  Olins, Peter O.
;                  Paik, Kumnan
;                  Thomas, John W.
;       TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
;                           Fusion Protein
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
;                       Corporate Patent Dept.
;            STREET: P. O. Box 5110
;            CITY: Chicago
;            STATE: Illinois
;            COUNTRY: USA
;            ZIP: 60680
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/08/762,227A
;            FILING DATE: 09-Dec-1996
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US 08/192,325
;            FILING DATE: 14-FEB-1994
;            APPLICATION NUMBER: US 08/446,872
;            FILING DATE: 06-JUN-1995
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bennett, Dennis A.
;            REGISTRATION NUMBER: 34,547
;            REFERENCE/DOCKET NUMBER: C-2790/5
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (708)470-6501
;            TELEFAX: (708)470-6881
;  INFORMATION FOR SEQ ID NO: 69:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 822 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA (genomic)
;       SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-08-762-227A-69

Alignment Scores:
Pred. No.:              6.6e-76         Length:         822
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     3               Gaps:           0

US-10-723-083-2 (1-142) x US-08-762-227A-69 (1-822)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
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Db        439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 498

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 558

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
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Db        559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 618

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet  94
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 678

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
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Db        739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 798

Qy        135 AspCysTrpGluProValGlnGlu 142
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Db        799 GACTGCTGGGAGCCAGTCCAGGAG 822

RESULT 15
PCT-US95-01185-69
; Sequence 69, Application PC/TUS9501185
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Multivariant IL-3 Hematopoiesis Fusion
;    TITLE OF INVENTION:  Protein
;    NUMBER OF SEQUENCES:  196
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/01185
;      FILING DATE:  02-FEB-1995
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/192325
;      FILING DATE:  14-FEB-1994
;  INFORMATION FOR SEQ ID NO:  69:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  822 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
PCT-US95-01185-69

Alignment Scores:
Pred. No.:              6.6e-76         Length:         822
Score:                  678.00          Matches:        128
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 88.63% Indels: 0
DB: 5 Gaps: 0

US-10-723-083-2 (1-142) x PCT-US95-01185-69 (1-822)

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Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
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Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
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Db        619 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 678

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
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Db        679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        135 AspCysTrpGluProValGlnGlu 142
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Db        799 GACTGCTGGGAGCCAGTCCAGGAG 822
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Job time : 167 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2005, 19:37:32 ; Search time 505 Seconds
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Title: US-10-723-083-2
Perfect score: 765
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 5537552 seqs, 2974263231 residues

Total number of hits satisfying chosen parameters: 11075104

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool/US10723083/runat_08032005_131719_10538/app_query.fasta_1.327
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10723083_@CGN_1_1_680_@runat_08032005_131719_10538
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-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
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Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	765	100.0	429	19	US-10-723-083-3	Sequence 3, Appli
2	765	100.0	458	19	US-10-723-083-1	Sequence 1, Appli
3	682	89.2	777	16	US-10-083-446-55	Sequence 55, Appl
4	678	88.6	402	16	US-10-083-446-176	Sequence 176, App
5	678	88.6	822	16	US-10-083-446-69	Sequence 69, Appl
6	678	88.6	903	16	US-10-083-446-66	Sequence 66, Appl
7	675	88.2	2211	17	US-10-609-346-9	Sequence 9, Appli
8	673	88.0	429	17	US-10-449-831A-141	Sequence 141, App
9	673	88.0	435	9	US-09-826-025-8	Sequence 8, Appli
10	673	88.0	435	14	US-10-083-590-14	Sequence 14, Appl
11	673	88.0	435	17	US-10-188-056-31	Sequence 31, Appl
12	673	88.0	435	17	US-10-188-056-32	Sequence 32, Appl
13	673	88.0	435	17	US-10-411-037-17	Sequence 17, Appl
14	673	88.0	435	17	US-10-411-026-17	Sequence 17, Appl
15	673	88.0	435	17	US-10-410-962-17	Sequence 17, Appl
16	673	88.0	435	17	US-10-411-049-17	Sequence 17, Appl
17	673	88.0	435	18	US-10-410-930-17	Sequence 17, Appl
18	673	88.0	435	18	US-10-410-997-17	Sequence 17, Appl
19	673	88.0	435	18	US-10-411-012-17	Sequence 17, Appl
20	673	88.0	435	18	US-10-287-994-17	Sequence 17, Appl
21	673	88.0	435	18	US-10-410-913-17	Sequence 17, Appl
22	673	88.0	435	18	US-10-785-577-8	Sequence 8, Appli
23	673	88.0	435	19	US-10-410-980-17	Sequence 17, Appl
24	673	88.0	448	17	US-10-609-346-19	Sequence 19, Appl
25	673	88.0	505	18	US-10-688-845-82	Sequence 82, Appl
26	673	88.0	579	17	US-10-449-831A-187	Sequence 187, App
27	673	88.0	781	17	US-10-447-315-20	Sequence 20, Appl
28	673	88.0	789	16	US-10-131-985-16	Sequence 16, Appl
29	673	88.0	789	19	US-10-901-417-16	Sequence 16, Appl
30	673	88.0	1011	13	US-10-044-090-509	Sequence 509, App
31	673	88.0	1318	14	US-10-228-811-3	Sequence 3, Appli
32	673	88.0	1833	9	US-09-783-708-2	Sequence 2, Appli
33	673	88.0	2070	9	US-09-821-883-7	Sequence 7, Appli
34	669	87.5	767	18	US-10-666-122-4	Sequence 4, Appli
35	669	87.5	767	18	US-10-666-122-6	Sequence 6, Appli
36	669	87.5	767	19	US-10-278-698-30	Sequence 30, Appl
37	669	87.5	767	19	US-10-278-698-544	Sequence 544, App
38	668	87.3	381	9	US-09-821-883-19	Sequence 19, Appl
39	668	87.3	435	17	US-10-188-056-33	Sequence 33, Appl
40	668	87.3	435	17	US-10-188-056-34	Sequence 34, Appl
41	668	87.3	496	16	US-10-267-384-191	Sequence 191, App
42	668	87.3	737	15	US-10-081-969-19	Sequence 19, Appl
43	668	87.3	756	15	US-10-177-390-21	Sequence 21, Appl
44	668	87.3	756	17	US-10-351-157-180	Sequence 180, App
45	668	87.3	756	17	US-10-352-554-165	Sequence 165, App

ALIGNMENTS

RESULT 1
US-10-723-083-3
; Sequence 3, Application US/10723083
; Publication No. US20050050602A1
; GENERAL INFORMATION:
; APPLICANT: Altosaar, Illimar
; APPLICANT: Sardana, Ravinder
; APPLICANT: Dudani, Aail
; APPLICANT: Ganz, Peter
; APPLICANT: Tackaberry, Eilleen
; TITLE OF INVENTION: Production of GM-CSF in Plants
; FILE REFERENCE: 08-898901US
; CURRENT APPLICATION NUMBER: US/10/723,083
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: Canada 2,410,702
; PRIOR FILING DATE: 2002-11-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 429

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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(429)
;   OTHER INFORMATION:
US-10-723-083-3

Alignment Scores:
Pred. No.:              2.88e-92        Length:         429
Score:                  765.00          Matches:        142
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     19              Gaps:           0

US-10-723-083-2 (1-142) x US-10-723-083-3 (1-429)

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Db          1 ATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCACCCGCCCGGTCA 60

Qy         21 ProSerProSerThrGlnProTrpGluHisValAsnAlaIleGlnGluAlaArgArgLeu 40
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Db         61 CCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTCTC 120

Qy         41 LeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGluValIleSerGlu 60
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Db        121 CTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTGATATCAGAA 180

Qy         61 MetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeuTyrLysGlnGly 80
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Db        181 ATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGC 240

Qy         81 LeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAlaSerHisTyrLys 100
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Qy        121 PheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAspCysTrpGluProVal 140
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Qy        141 GlnGlu 142
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RESULT 2
US-10-723-083-1
; Sequence 1, Application US/10723083
; Publication No. US20050050602A1
; GENERAL INFORMATION:
;  APPLICANT: Altosaar, Illimar
;  APPLICANT:  Sardana, Ravinder
;  APPLICANT:  Dudani, Aail
;  APPLICANT:  Ganz, Peter
;  APPLICANT:  Tackaberry, Eilleen
;  TITLE OF INVENTION: Production of GM-CSF in Plants
;  FILE REFERENCE: 08-898901US
;  CURRENT APPLICATION NUMBER: US/10/723,083
;  CURRENT FILING DATE:  2003-11-26
;  PRIOR APPLICATION NUMBER: Canada 2,410,702
;  PRIOR FILING DATE: 2002-11-26
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 458
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (10)..(438)
;   OTHER INFORMATION:
US-10-723-083-1

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Score:                  765.00          Matches:        142
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     19              Gaps:           0

US-10-723-083-2 (1-142) x US-10-723-083-1 (1-458)

Qy          1 MetHisHisHisHisHisSerSerGlyIleGluGlyArgMetAlaProAlaArgSer 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 ATGCACCACCACCACCACCACTCCTCCGGCATCGAGGGCCGCATGGCACCCGCCCGGTCA 69

Qy         21 ProSerProSerThrGlnProTrpGluHisValAsnAlaIleGlnGluAlaArgArgLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAGGCCCGGCGTCTC 129

Qy         41 LeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGluValIleSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 CTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTGATATCAGAA 189

Qy         61 MetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeuTyrLysGlnGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 ATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGC 249

Qy         81 LeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAlaSerHisTyrLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CTCCGCGGCAGCCTCACCAAGCTCAAGGGCCCGCTCACCATGATGGCGTCCCACTACAAG 309

Qy        101 GlnHisCysProProThrProGluThrSerCysAlaThrGlnIleIleThrPheGluSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CAGCACTGCCCACCGACCCCGGAGACCTCCTGCGCCACCCAGATCATCACCTTCGAGAGC 369

Qy        121 PheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAspCysTrpGluProVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 TTCAAGGAGAACCTCAAGGACTTCCTCCTCGTGATCCCGTTCGACTGCTGGGAGCCGGTG 429

Qy        141 GlnGlu 142
              ||||||
Db        430 CAGGAG 435

RESULT 3
US-10-083-446-55
; Sequence 55, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;       APPLICANT: Abrams, Mark A.
;                  Bauer, S. C.
;                  Braford-Goldberg, Sarah R.
;                  Caparon, Maire H.
;                  Easton, Alan M.
;                  Klein, Barbara K.
;                  McKearn, John P.
;                  Olins, Peter O.
;                  Paik, Kumnan
;                  Thomas, John W.
;       TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                           Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;       NUMBER OF SEQUENCES: 197
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                      Corporate Patent Dept., Mail Zone 04E
;           STREET: 800 N. Lindbergh
;           CITY: St. Louis
;           STATE: Missouri
;           COUNTRY: USA
;           ZIP: 63167
```

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;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/083,446
;             FILING DATE: 26-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/762,227
;             FILING DATE: 09-DEC-1996
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: S. Christopher Bauer
;             REGISTRATION NUMBER: 42,305
;             REFERENCE/DOCKET NUMBER: C-2790/6
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (636)737-6257
;             TELEFAX: (636)737-5452
;    INFORMATION FOR SEQ ID NO: 55:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 777 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-083-446-55

Alignment Scores:
Pred. No.:              8.04e-81        Length:         777
Score:                  682.00          Matches:        130
Percent Similarity:     97.01%          Conservative:   0
Best Local Similarity:  97.01%          Mismatches:     4
Query Match:            89.15%          Indels:         0
DB:                     16              Gaps:           0

US-10-723-083-2 (1-142) x US-10-083-446-55 (1-777)

Qy          9 SerGlyIleGluGlyArgMetAlaProAlaArgSerProSerProSerThrGlnProTrp 28
              ||||||              ||||||||||||||||||||||||||||||||||||||||||
Db        376 TCTGGCGGCGGCTCCAACATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGG 435

Qy         29 GluHisValAsnAlaIleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAla 48
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GAACACGTGAATGCCATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCT 495

Qy         49 AlaGluMetAsnGluThrValGluValIleSerGluMetPheAspLeuGlnGluProThr 68
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 GCTGAGATGAATGAAACAGTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACT 555

Qy         69 CysLeuGlnThrArgLeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeu 88
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTC 615

Qy         89 LysGlyProLeuThrMetMetAlaSerHisTyrLysGlnHisCysProProThrProGlu 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AAGGGCCCCTTGACCATGATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAA 675

Qy        109 ThrSerCysAlaThrGlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPhe 128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        676 ACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTC 735

Qy        129 LeuLeuValIleProPheAspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||||||||||||||||||||
Db        736 CTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTCCAGGAG 777

RESULT 4
US-10-083-446-176
```

```
; Sequence 176, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Thomas, John W.
;        TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                            Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;        NUMBER OF SEQUENCES: 197
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                        Corporate Patent Dept., Mail Zone O4E
;             STREET: 800 N. Lindbergh
;             CITY: St. Louis
;             STATE: Missouri
;             COUNTRY: USA
;             ZIP: 63167
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/083,446
;             FILING DATE: 26-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/762,227
;             FILING DATE: 09-DEC-1996
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: S. Christopher Bauer
;             REGISTRATION NUMBER: 42,305
;             REFERENCE/DOCKET NUMBER: C-2790/6
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (636)737-6257
;             TELEFAX: (636)737-5452
;    INFORMATION FOR SEQ ID NO: 176:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 402 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 176:
US-10-083-446-176

Alignment Scores:
Pred. No.:              1.1e-80         Length:         402
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     16              Gaps:           0

US-10-723-083-2 (1-142) x US-10-083-446-176 (1-402)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 60

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         61 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 120

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 180

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 240

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 300

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 360

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        361 GACTGCTGGGAGCCAGTCCAGGAG 384

RESULT 5
US-10-083-446-69
; Sequence 69, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Thomas, John W.
;        TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                            Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;        NUMBER OF SEQUENCES: 197
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                        Corporate Patent Dept., Mail Zone O4E
;             STREET: 800 N. Lindbergh
;             CITY: St. Louis
;             STATE: Missouri
;             COUNTRY: USA
;             ZIP: 63167
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/083,446
;             FILING DATE: 26-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/762,227
;             FILING DATE: 09-DEC-1996
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: S. Christopher Bauer
;             REGISTRATION NUMBER: 42,305
;             REFERENCE/DOCKET NUMBER: C-2790/6
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (636)737-6257
;             TELEFAX: (636)737-5452
;   INFORMATION FOR SEQ ID NO: 69:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 822 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-10-083-446-69

Alignment Scores:
Pred. No.:              2.98e-80        Length:         822
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     16              Gaps:           0

US-10-723-083-2 (1-142) x US-10-083-446-69 (1-822)

Qy         15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 498

Qy         35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 558

Qy         55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        559 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 618

Qy         75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 678

Qy         95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        679 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 738

Qy        115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        739 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 798

Qy        135 AspCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        799 GACTGCTGGGAGCCAGTCCAGGAG 822

RESULT 6
US-10-083-446-66
; Sequence 66, Application US/10083446
; Publication No. US20030185790A1
;   GENERAL INFORMATION:
;        APPLICANT: Abrams, Mark A.
;                   Bauer, S. C.
;                   Braford-Goldberg, Sarah R.
;                   Caparon, Maire H.
;                   Easton, Alan M.
;                   Klein, Barbara K.
;                   McKearn, John P.
;                   Olins, Peter O.
;                   Paik, Kumnan
;                   Thomas, John W.
;        TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
;                            Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
;        NUMBER OF SEQUENCES: 197
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
;                        Corporate Patent Dept., Mail Zone O4E
;             STREET: 800 N. Lindbergh
;             CITY: St. Louis
;             STATE: Missouri
;             COUNTRY: USA
;             ZIP: 63167
;        COMPUTER READABLE FORM:
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```
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/083,446
;             FILING DATE: 26-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/762,227
;             FILING DATE: 09-DEC-1996
;             APPLICATION NUMBER: US 08/192,325
;             FILING DATE: 14-FEB-1994
;             APPLICATION NUMBER: US 08/446,872
;             FILING DATE: 06-JUN-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: S. Christopher Bauer
;             REGISTRATION NUMBER: 42,305
;             REFERENCE/DOCKET NUMBER: C-2790/6
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (636)737-6257
;             TELEFAX: (636)737-5452
;    INFORMATION FOR SEQ ID NO: 66:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 903 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-083-446-66

Alignment Scores:
Pred. No.:              3.39e-80        Length:         903
Score:                  678.00          Matches:        128
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.63%          Indels:         0
DB:                     16              Gaps:           0

US-10-723-083-2 (1-142) x US-10-083-446-66 (1-903)

Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         520 ATGGCACCGGCTCGTTCCCCGTCCCCGTCTACCCAGCCGTGGGAACACGTGAATGCCATC 579

Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         580 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 639

Qy          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         640 GTAGAAGTGATATCAGAAATGTTTGACCTCCAGGAGCCGACTTGCCTACAGACCCGCCTG 699

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         700 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 759

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         760 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 819

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         820 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTCCTGCTTGTCATCCCCTTT 879

Qy         135 AspCysTrpGluProValGlnGlu 142
               |||||||||||||||||||||||
Db         880 GACTGCTGGGAGCCAGTCCAGGAG 903

RESULT 7
US-10-609-346-9
; Sequence 9, Application US/10609346
; Publication No. US20040063635A1
; GENERAL INFORMATION:
;  APPLICANT: Yu, Zailin
;  APPLICANT:  Fu, Yan
;  TITLE OF INVENTION: RECOMBINANT HUMAN ALBUMIN FUSION PROTEINS WITH LONG-LASTING BIOLO
;  TITLE OF INVENTION:  EFFECTS
;  FILE REFERENCE: ZYU-0603
;  CURRENT APPLICATION NUMBER: US/10/609,346
;  CURRENT FILING DATE:  2003-06-26
;  PRIOR APPLICATION NUMBER: US 60/392,948
;  PRIOR FILING DATE: 2002-07-01
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
;   LENGTH: 2211
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: DNA of HSA-GMCSF
US-10-609-346-9

Alignment Scores:
Pred. No.:              2.98e-79        Length:         2211
Score:                  675.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  99.22%          Mismatches:     0
Query Match:            88.24%          Indels:         0
DB:                     17              Gaps:           0

US-10-723-083-2 (1-142) x US-10-609-346-9 (1-2211)

Qy          15 MetAlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIle 34
               :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1825 TTAGCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATC 1884

Qy          35 GlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThr 54
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1885 CAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACA 1944

Qy          55 ValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeu 74
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1945 GTAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTG 2004

Qy          75 GluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMet 94
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2005 GAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATG 2064

Qy          95 MetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGln 114
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2065 ATGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAG 2124

Qy         115 IleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPhe 134
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        2125 ATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTT 2184

Qy         135 AspCysTrpGluProValGlnGlu 142
               |||||||||||||||||||||||
Db        2185 GACTGCTGGGAGCCAGTCCAGGAG 2208

RESULT 8
US-10-449-831A-141
; Sequence 141, Application US/10449831A
; Publication No. US20040029179A1
; GENERAL INFORMATION:
;  APPLICANT: Koentgen, Frank
;  TITLE OF INVENTION: Higher molecular weight entities and uses therefor
;  FILE REFERENCE: 2385978
;  CURRENT APPLICATION NUMBER: US/10/449,831A
;  CURRENT FILING DATE:  2003-05-30
;  PRIOR APPLICATION NUMBER: USSN 60/384878
;  PRIOR FILING DATE: 2002-05-31
;  NUMBER OF SEQ ID NOS: 237
;  SOFTWARE: PatentIn version 3.2
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; SEQ ID NO 141
;   LENGTH: 429
;   TYPE: DNA
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(429)
US-10-449-831A-141

Alignment Scores:
Pred. No.:              5.58e-80        Length:         429
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     17              Gaps:           0

US-10-723-083-2 (1-142) x US-10-449-831A-141 (1-429)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         49 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 108

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 168

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        169 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 228

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        229 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 288

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        289 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 348

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        349 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 408

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        409 TGCTGGGAGCCAGTCCAGGAG 429

RESULT 9
US-09-826-025-8
; Sequence 8, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 8:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 435 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-826-025-8

Alignment Scores:
Pred. No.:              5.69e-80        Length:         435
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     9               Gaps:           0

US-10-723-083-2 (1-142) x US-09-826-025-8 (1-435)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 111

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 171

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 231

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 291

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 351

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 411

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        412 TGCTGGGAGCCAGTCCAGGAG 432

RESULT 10
US-10-083-590-14
; Sequence 14, Application US/10083590
; Publication No. US20030027257A1
; GENERAL INFORMATION:
;  APPLICANT: IATROU, Kostas
;  APPLICANT:  FARRELL, Patrick J.
;  APPLICANT:  BEHIE, Leo A.
;  TITLE OF INVENTION: SEQUENCES FOR IMPROVING THE EFFICIENCY OF SECRETION OF
;  TITLE OF INVENTION:  NON-SECRETED PROTEINS FROM MAMMALIAN AND INSECT CELLS
;  FILE REFERENCE: 028722-207
;  CURRENT APPLICATION NUMBER: US/10/083,590
;  CURRENT FILING DATE:  2002-02-27
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/256,694
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-24
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/136,421
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;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/056,871
;  PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-21
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Human
US-10-083-590-14

Alignment Scores:
Pred. No.:              5.69e-80        Length:         435
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     14              Gaps:           0

US-10-723-083-2 (1-142) x US-10-083-590-14 (1-435)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 111

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 171

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 231

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 291

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 351

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 411

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        412 TGCTGGGAGCCAGTCCAGGAG 432

RESULT 11
US-10-188-056-31
; Sequence 31, Application US/10188056
; Publication No. US20040009934A1
; GENERAL INFORMATION:
;  APPLICANT: Qiu, Jian-Tai
;  APPLICANT:  Lai, Wan-Ching
;  APPLICANT:  Chu, Yong Liang
;  APPLICANT:  Li, Frank Q.
;  TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
;  FILE REFERENCE: 3781-004-27
;  CURRENT APPLICATION NUMBER: US/10/188,056
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 31
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-188-056-31

Alignment Scores:
Pred. No.:              5.69e-80        Length:         435
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     17              Gaps:           0

US-10-723-083-2 (1-142) x US-10-188-056-31 (1-435)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 GCTCCCGCCAGAAGCCCCAGCCCCTCCACCCAGCCCTGGGAGCACGTGAACGCCATCCAG 111

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GAGGCCAGACGGCTGCTGAACCTGTCCAGAGACACCGCCGCCGAGATGAACGAGACCGTG 171

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GAGGTGATCAGCGAGATGTTCGACCTGCAGGAGCCCACCTGTCTGCAGACCCGGCTGGAG 231

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CTGTACAAGCAGGGACTGCGGGGCAGCCTGACCAAGCTGAAGGGACCCCTGACCATGATG 291

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GCCAGCCACTACAAGCAGCACTGCCCTCCCACACCCGAGACCAGCTGCGCCACCCAGATC 351

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 ATCACCTTCGAGAGCTTCAAGGAGAACCTGAAGGACTTCCTGCTGGTGATCCCCTTCGAC 411

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        412 TGCTGGGAGCCCGTGCAGGAG 432

RESULT 12
US-10-188-056-32
; Sequence 32, Application US/10188056
; Publication No. US20040009934A1
; GENERAL INFORMATION:
;  APPLICANT: Qiu, Jian-Tai
;  APPLICANT:  Lai, Wan-Ching
;  APPLICANT:  Chu, Yong Liang
;  APPLICANT:  Li, Frank Q.
;  TITLE OF INVENTION: Improved GM-CSF Nucleic Acid Sequences
;  FILE REFERENCE: 3781-004-27
;  CURRENT APPLICATION NUMBER: US/10/188,056
;  CURRENT FILING DATE:  2002-09-26
;  NUMBER OF SEQ ID NOS: 34
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-188-056-32

Alignment Scores:
Pred. No.:              5.69e-80        Length:         435
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     17              Gaps:           0

US-10-723-083-2 (1-142) x US-10-188-056-32 (1-435)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 GCACCCGCCCGCTCGCCCAGCCCCAGCACACAGCCCTGGGAGCATGTGAATGCCATCCAG 111

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 171
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Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 231

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 291

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GCCAGCCACTACAAACAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 351

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 411

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        412 TGCTGGGAGCCAGTCCAGGAG 432

RESULT 13
US-10-411-037-17
; Sequence 17, Application US/10411037
; Publication No. US20040043446A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
;  TITLE OF INVENTION:  GALACTOSIDASE A
;  FILE REFERENCE: 040853-01-5082
;  CURRENT APPLICATION NUMBER: US/10/411,037
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-411-037-17

Alignment Scores:
Pred. No.:              5.69e-80        Length:         435
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     17              Gaps:           0

US-10-723-083-2 (1-142) x US-10-411-037-17 (1-435)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 111

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 171

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 231

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 291

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 351

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 411

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        412 TGCTGGGAGCCAGTCCAGGAG 432

RESULT 14
US-10-411-026-17
; Sequence 17, Application US/10411026
; Publication No. US20040063911A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE
;  TITLE OF INVENTION:  METHODS
;  FILE REFERENCE: 040853-01-5053
;  CURRENT APPLICATION NUMBER: US/10/411,026
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-411-026-17

Alignment Scores:
Pred. No.:              5.69e-80        Length:         435
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     17              Gaps:           0

US-10-723-083-2 (1-142) x US-10-411-026-17 (1-435)
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```
Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 111

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 171

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 231

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 291

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 351

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 411

Qy        136 CysTrpGluProValGlnGlu 142
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Db        412 TGCTGGGAGCCAGTCCAGGAG 432
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RESULT 15
US-10-410-962-17
; Sequence 17, Application US/10410962
; Publication No. US20040077836A1
; GENERAL INFORMATION:
;  APPLICANT: Neose Technologies, Inc.
;  APPLICANT:  DeFrees, Shawn
;  APPLICANT:  Zopf, David
;  APPLICANT:  Bayer, Robert
;  APPLICANT:  Hakes, David
;  APPLICANT:  Chen, Xi
;  APPLICANT:  Bowe, Caryn
;  TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND
;  TITLE OF INVENTION:  GLYCOCONJUGATION OF G-CSF
;  FILE REFERENCE: 040853-01-5054
;  CURRENT APPLICATION NUMBER: US/10/410,962
;  CURRENT FILING DATE:  2003-04-09
;  PRIOR APPLICATION NUMBER: US 60/328,523
;  PRIOR FILING DATE: 2001-10-10
;  PRIOR APPLICATION NUMBER: US 60/344,692
;  PRIOR FILING DATE: 2001-10-19
;  PRIOR APPLICATION NUMBER: US 60/387,292
;  PRIOR FILING DATE: 2002-06-07
;  PRIOR APPLICATION NUMBER: US 60/391,777
;  PRIOR FILING DATE: 2002-06-25
;  PRIOR APPLICATION NUMBER: US 60/396,594
;  PRIOR FILING DATE: 2002-07-17
;  PRIOR APPLICATION NUMBER: US 60/404,249
;  PRIOR FILING DATE: 2002-08-16
;  PRIOR APPLICATION NUMBER: US 60/407,527
;  PRIOR FILING DATE: 2002-08-28
;  NUMBER OF SEQ ID NOS: 75
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
;   LENGTH: 435
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-410-962-17

Alignment Scores:
Pred. No.:              5.69e-80        Length:         435
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
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DB:                     17              Gaps:           0

US-10-723-083-2 (1-142) x US-10-410-962-17 (1-435)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 111

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 171

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 231

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 291

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 351

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 411

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        412 TGCTGGGAGCCAGTCCAGGAG 432
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Search completed: March 11, 2005, 21:35:24
Job time : 512 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: March 11, 2005, 18:16:26 ; Search time 2822 Seconds
(without alignments)
1915.353 Million cell updates/sec

Title: US-10-723-083-2
Perfect score: 765
Sequence: 1 MHHHHHHSSGIEGRMAPARS.....ENLKDFLLVIPFDCWEPVQE 142

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US10723083/runat_08032005_131716_10436/app_query.fasta_1.327
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10723083_@CGN_1_1_4352_@runat_08032005_131716_10436 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	673	88.0	588	2	AW207707	AW207707 UI-H-BI2-
c	2	673	88.0	658	5	BX111836	BX111836 BX111836
	3	673	88.0	660	2	BE218982	BE218982 hv47a07.x
	4	673	88.0	666	1	AI912784	AI912784 we13f07.x
	5	673	88.0	672	2	BE671554	BE671554 7e53h07.x
	6	673	88.0	695	2	BE669962	BE669962 7e27g08.x
	7	673	88.0	895	2	BE873976	BE873976 601484045
	8	668	87.3	584	7	CF341802	CF341802 TgESTzyj4
	9	652	85.2	592	7	CF370966	CF370966 TgESTzyj5
	10	647	84.6	565	2	BF938995	BF938995 7r03f11.x
	11	647	84.6	585	7	CF370833	CF370833 TgESTzyj5
c	12	640	83.7	718	6	CD369973	CD369973 UI-H-FT1-
c	13	614	80.3	701	5	BU633411	BU633411 UI-H-FL1-
c	14	563	73.6	666	6	CA307828	CA307828 UI-H-FT1-
	15	559	73.1	475	1	AA995402	AA995402 or74f05.s
c	16	534	69.8	661	6	CD368851	CD368851 UI-H-FT1-
	17	480.5	62.8	561	6	CB457551	CB457551 714908 MA
	18	480.5	62.8	672	7	CF614774	CF614774 CES009198
	19	473	61.8	572	4	BM539160	BM539160 hb05e10.g
	20	469.5	61.4	511	6	CB430266	CB430266 606148 MA
	21	458	59.9	336	2	AW951121	AW951121 EST363191
c	22	453	59.2	608	6	CD367244	CD367244 UI-H-FT2-
	23	419	54.8	423	2	AW784714	AW784714 zb77g08.g
c	24	402	52.5	549	1	AI677936	AI677936 wc88f12.x
c	25	375	49.0	531	4	BG236310	BG236310 naf26a07.
	26	343	44.8	274	1	AA361936	AA361936 EST71529
	27	301.5	39.4	647	2	BB533718	BB533718 BB533718
	28	269.5	35.2	629	2	BB664267	BB664267 BB664267
	29	268	35.0	269	7	CF370885	CF370885 TgESTzyj5
c	30	260	34.0	517	6	CB430980	CB430980 606916 MA
	31	254	33.2	369	5	BX521029	BX521029 BX521029
	32	248	32.4	483	1	AI180669	AI180669 uc47d08.r
c	33	245	32.0	244	4	BG236058	BG236058 naf21h12.
	34	229	29.9	470	1	AI121878	AI121878 ud13c11.r
	35	214	28.0	697	9	AG112609	AG112609 Pan trogl
	36	171	22.4	160	7	CF341980	CF341980 TgESTzyj5
	37	162	21.2	136	7	CF341168	CF341168 TgESTzyj4
c	38	157	20.5	892	9	CR059250	CR059250 Forward s
	39	102	13.3	935	7	CF264246	CF264246 AGENCOURT
c	40	101	13.2	721	8	AZ969504	AZ969504 2M0242J17
	41	99.5	13.0	131	8	AF179193	AF179193 AF179193
c	42	98	12.8	372	7	T29160	T29160 EST71528 Hu
	43	94	12.3	828	7	CK144209	CK144209 AGENCOURT
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c	45	91.5	12.0	699	1	AJ819401	AJ819401 AJ819401

ALIGNMENTS

RESULT 1
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LOCUS AW207707 588 bp mRNA linear EST 02-DEC-1999
DEFINITION UI-H-BI2-age-e-09-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens cDNA clone IMAGE:2724184 3', mRNA sequence.
ACCESSION AW207707
VERSION AW207707.1 GI:6507203
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 588)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=No.
FEATURES Location/Qualifiers
source 1. .588
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2724184"
/lab_host="DH10B (Life Technologies)"

/clone_lib="NCI_CGAP_Sub4"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NCI_CGAP_Sub4 library is a subtracted library derived from the NCI_CGAP_Sub2 library which is a subtracted library derived from the NCI_CGAP_Sub1 library, which is a subtracted library derived from BI. BI constitutes a mixture of 21 normalized or subtracted NCI_CGAP libraries: NCI_CGAP_Co4, NCI_CGAP_Pr22, NCI_CGAP_Pr28, NCI_CGAP_Co10, NCI_CGAP_Co16, NCI_CGAP_Kid5, NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11, NCI_CGAP_Lym2, NCI_CGAP_Br2, NCI_CGAP_Co8, NCI_CGAP_CLL1, NCI_CGAP_Lei2, NCI_CGAP_Brn23, NCI_CGAP_Lu5, NCI_CGAP_Lu24, NCI_CGAP_Lu19, NCI_CGAP_GC4, NCI_CGAP_GC6, NCI_CGAP_Brn25. These 21 libraries were pooled and a single-stranded DNA preparation of the resulting mixture was used as a tracer in a subtractive hybridization with a driver whose composition is detailed below: NCI_CGAP_Kid3 pool 1 : LLAM 3334-3337, 3682-3683, 3798-3803 (IMAGE CloneIDs 1322376-1323911, 1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 : LLAM 3338-3342, 3722-3725, 3776-3778 (IMAGE CloneIDs 1323912-1325831, 1471368-1472903, 1492104-1493255) NCI_CGAP_Lu5 pool 1 : LLAM 3575-3582, 3851-3854 (IMAGE CloneIDs 1414920-1417991, 1520904-1522439) NCI_CGAP_GC4 pool 1 : LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDs 1257096-1258631, 1469064-1470983, 1475592-1476743) NCI_CGAP_Pr22 pool 1 : LLAM 2457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDs 985608-986759, 1101192-1101959, 1217928-1220615) NCI_CGAP_Co10 pool 1 : LLAM 2644-2653, 2871-2872 (IMAGE CloneIDs 1057416-1061255, 1144584-1145351) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]
TAG_TISSUE=colon
TAG_LIB=NCI_CGAP_Co4
TAG_SEQ=CTTCG"

ORIGIN

Alignment Scores:

Pred. No.:	5.9e-63	Length:	588
Score:	673.00	Matches:	127
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	87.97%	Indels:	0
DB:	2	Gaps:	0

US-10-723-083-2 (1-142) x AW207707 (1-588)

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Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
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Db         88 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 147

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        148 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 207

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
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Db        208 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 267

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
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Db        268 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 327

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 387

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 447
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Qy        136 CysTrpGluProValGlnGlu 142
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Db        448 TGCTGGGAGCCAGTCCAGGAG 468
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RESULT 2
BX111836/c

LOCUS	BX111836 658 bp mRNA linear EST 07-FEB-2003
DEFINITION	BX111836 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGp998C104061 ; IMAGE:1601601, mRNA sequence.
ACCESSION	BX111836
VERSION	BX111836.1 GI:27837278
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 658)
AUTHORS	Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M., Radelof,U., Schneider,D. and Korn,B.
TITLE	Human UnigeneSet - RZPD3
JOURNAL	Unpublished (2003)
COMMENT	Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany RZPD; IMAGp998C104061. RZPDLIB; I.M.A.G.E. cDNA Clone Collection; Human UnigeneSet - RZPD3 (RZPDLIB No.972) http://www.rzpd.de/CloneCards/cgi-bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany Tel: +49 30 32639 101 Fax: +49 30 32639 111 www.rzpd.de This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seq primer: M13r, Primer sequence: TTTCACACAGGAAACAGCTATGAC.

FEATURES Location/Qualifiers

source 1. .658
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/db_xref="taxon:9606"
/clone="IMAGp998C104061 ; IMAGE:1601601"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu5"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	6.86e-63	Length:	658
Score:	673.00	Matches:	127
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	87.97%	Indels:	0
DB:	5	Gaps:	0

US-10-723-083-2 (1-142) x BX111836 (1-658)

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Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
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Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
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Db        559 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 500

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        499 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 440

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        439 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 380

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        379 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 320

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        319 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 260

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        259 TGCTGGGAGCCAGTCCAGGAG 239

RESULT 3
BE218982
LOCUS       BE218982                660 bp    mRNA    linear   EST 03-JUL-2000
DEFINITION  hv47a07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3176532 3'
            similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
            FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   BE218982
VERSION     BE218982.1  GI:8906300
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 445.
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                     /clone_lib="NCI_CGAP_Lu24"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
                     clones made from the same library (cloneIDs
                     1414920-1417991 and 1520904-1522439). Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
ORIGIN

Alignment Scores:

Pred. No.:                6.88e-63      Length:          660
Score:                    673.00        Matches:         127
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              87.97%        Indels:          0
DB:                       2             Gaps:            0

US-10-723-083-2 (1-142) x BE218982 (1-660)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 115

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 175

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 235

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 295

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 355

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 415

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        416 TGCTGGGAGCCAGTCCAGGAG 436

RESULT 4
AI912784
LOCUS       AI912784                666 bp    mRNA    linear   EST 18-DEC-1999
DEFINITION  we13f07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:2340997 3'
            similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
            FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AI912784
VERSION     AI912784.1  GI:5632639
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 743    Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 447.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/clone="IMAGE:2340997"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	6.97e-63	Length:	666
Score:	673.00	Matches:	127
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	87.97%	Indels:	0
DB:	1	Gaps:	0

US-10-723-083-2 (1-142) x AI912784 (1-666)

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Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         56 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 115

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 175

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 235

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        236 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 295

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        296 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 355

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 415

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        416 TGCTGGGAGCCAGTCCAGGAG 436
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RESULT 5
BE671554
LOCUS BE671554 672 bp mRNA linear EST 08-SEP-2000
DEFINITION 7e53h07.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3286237 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION BE671554
VERSION BE671554.1 GI:10032095
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 672)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 440.
FEATURES Location/Qualifiers
source 1. .672
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3286237"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Alignment Scores:

Pred. No.:	7.05e-63	Length:	672
Score:	673.00	Matches:	127
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	87.97%	Indels:	0
DB:	2	Gaps:	0

US-10-723-083-2 (1-142) x BE671554 (1-672)

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Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 122

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 182

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 242

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 302

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 362

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 422

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        423 TGCTGGGAGCCAGTCCAGGAG 443
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RESULT 6
BE669962
LOCUS BE669962 695 bp mRNA linear EST 08-SEP-2000
DEFINITION 7e27g08.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3283742 3' similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING

```
            FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   BE669962
VERSION     BE669962.1  GI:10030503
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 695)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 456.
FEATURES             Location/Qualifiers
     source          1. .695
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3283742"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu24"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
                     clones made from the same library (cloneIDs
                     1414920-1417991 and 1520904-1522439). Subtraction by Bento
                     Soares and M. Fatima Bonaldo.  "
ORIGIN

Alignment Scores:
Pred. No.:              7.38e-63        Length:         695
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     2               Gaps:           0

US-10-723-083-2 (1-142) x BE669962 (1-695)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         92 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 151

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 211

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 271

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 331

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        332 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 391

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 451

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        452 TGCTGGGAGCCAGTCCAGGAG 472

RESULT 7
BE873976
LOCUS       BE873976                895 bp    mRNA    linear   EST 20-OCT-2000
DEFINITION  601484045F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3886571 5',
            mRNA sequence.
ACCESSION   BE873976
VERSION     BE873976.1  GI:10322752
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 895)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP/Gazdar
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9663  row: j  column: 12
            High quality sequence stop: 711.
FEATURES             Location/Qualifiers
     source          1. .895
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3886571"
                     /tissue_type="large cell carcinoma, undifferentiated"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_69"
                     /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.  Library constructed by Life
                     Technologies."
ORIGIN

Alignment Scores:
Pred. No.:              1.03e-62        Length:         895
Score:                  673.00          Matches:        127
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            87.97%          Indels:         0
DB:                     2               Gaps:           0

US-10-723-083-2 (1-142) x BE873976 (1-895)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         50 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 109

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        110 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 169

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        170 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 229
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Qy          76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         230 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 289

Qy          96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         290 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATT 349

Qy         116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         350 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 409

Qy         136 CysTrpGluProValGlnGlu 142
               |||||||||||||||||||||
Db         410 TGCTGGGAGCCAGTCCAGGAG 430

RESULT 8
CF341802
LOCUS       CF341802                 584 bp    mRNA    linear   EST 18-AUG-2003
DEFINITION  TgESTzyj43f02.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
            cDNA clone TgESTzyj43f02.y1 5' similar to SW:CSF2_HUMAN P04141
            GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
            sequence.
ACCESSION   CF341802
VERSION     CF341802.1  GI:33831915
KEYWORDS    EST.
SOURCE      Toxoplasma gondii
  ORGANISM  Toxoplasma gondii
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
            Sarcocystidae; Toxoplasma.
REFERENCE   1  (bases 1 to 584)
  AUTHORS   Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
            Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
            Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
            Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
            Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
  TITLE     Toxoplasma EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Clifton, S.
            Toxoplasma EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: toxo@watson.wustl.edu
            Contact David Sibley (toxoest@borcim.wustl.edu) for further
            information relating to organism, libraries, or clone availability.
            Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .584
                     /organism="Toxoplasma gondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:5811"
                     /clone="TgESTzyj43f02.y1"
                     /dev_stage="Tachyzoite"
                     /lab_host="ElectroTen Blue cells (Stratagene)"
                     /clone_lib="Tg CAST Tachyzoite cDNA Library"
                     /note="Vector: Modified pBluescript (pBS SK+); Site_1:
                     BamH1; Site_2: EcoR1; The cDNA library was constructed by
                     Keliang Tang, and Robert Cole at Washington University.
                     cDNA was synthesized from poly(A)+ mRNA using the
                     template-switching PCR method (SMART cDNA Kit, BD
                     Biosciences). First strand cDNA was reverse transcribed
                     using the CDS III/3' primer and a 5' template switch
                     primer (Smart IV primer). The product of the first strand
                     synthesis was PCR amplified using the same primer set and
                     the fragments were digested with SfiI. The fragments were
                     size selected, ligated into a modified pBluescript vector
                     (obtained from Michael White, Montana State University)
                     containing directional SfiI sites, and electroporated into
                     ElectroTen Blue cells. Vector: SfiI sites were added to
                     the multiple cloning region of pBluescript SK+ between the
                     BamHI/EcoRI sites. The modified polylinker has the
                     following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--
                     GGCCGCCTCGGCCCACGGATCC3'where n=3-4 G nucleotides.
                     WARNING: the library contains a small percentage of cDNAs
                     derived from the human host cells. Library materials
                     provided by David Sibley, Washington University."
ORIGIN

Alignment Scores:
Pred. No.:                2.05e-62        Length:          584
Score:                    668.00          Matches:         126
Percent Similarity:       99.21%          Conservative:    0
Best Local Similarity:    99.21%          Mismatches:      1
Query Match:              87.32%          Indels:          0
DB:                       7               Gaps:            0

US-10-723-083-2 (1-142) x CF341802 (1-584)

Qy          16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          84 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 143

Qy          36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         144 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 203

Qy          56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         204 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 263

Qy          76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         264 CTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATG 323

Qy          96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         324 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGACT 383

Qy         116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         384 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 443

Qy         136 CysTrpGluProValGlnGlu 142
               |||||||||||||||||||||
Db         444 TGCTGGGAGCCAGTCCAGGAG 464

RESULT 9
CF370966
LOCUS       CF370966                 592 bp    mRNA    linear   EST 27-AUG-2003
DEFINITION  TgESTzyj58e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii
            cDNA clone TgESTzyj58e12.y1 5' similar to SW:CSF2_HUMAN P04141
            GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA
            sequence.
ACCESSION   CF370966
VERSION     CF370966.1  GI:34318212
KEYWORDS    EST.
SOURCE      Toxoplasma gondii
  ORGANISM  Toxoplasma gondii
            Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
            Sarcocystidae; Toxoplasma.
REFERENCE   1  (bases 1 to 592)
  AUTHORS   Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M.,
            Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
            Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M.,
            Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I.,
            Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
  TITLE     Toxoplasma EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Clifton, S.
            Toxoplasma EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
```

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           Fax: 314 286 1810
           Email: toxo@watson.wustl.edu
           Contact David Sibley (toxoest@borcim.wustl.edu) for further
           information relating to organism, libraries, or clone availability.
           Seq primer: -40UP from Gibco.
FEATURES             Location/Qualifiers
     source          1. .592
                     /organism="Toxoplasma gondii"
                     /mol_type="mRNA"
                     /db_xref="taxon:5811"
                     /clone="TgESTzyj58e12.y1"
                     /dev_stage="Tachyzoite"
                     /lab_host="ElectroTen Blue cells (Stratagene)"
                     /clone_lib="Tg CAST Tachyzoite cDNA Library"
                     /note="Vector: Modified pBluescript (pBS SK+); Site_1:
                     BamH1; Site_2: EcoR1; The cDNA library was constructed by
                     Keliang Tang, and Robert Cole at Washington University.
                     cDNA was synthesized from poly(A)+ mRNA using the
                     template-switching PCR method (SMART cDNA Kit, BD
                     Biosciences). First strand cDNA was reverse transcribed
                     using the CDS III/3' primer and a 5' template switch
                     primer (Smart IV primer). The product of the first strand
                     synthesis was PCR amplified using the same primer set and
                     the fragments were digested with SfiI. The fragments were
                     size selected, ligated into a modified pBluescript vector
                     (obtained from Michael White, Montana State University)
                     containing directional SfiI sites, and electroporated into
                     ElectroTen Blue cells. Vector: SfiI sites were added to
                     the multiple cloning region of pBluescript SK+ between the
                     BamHI/EcoRI sites. The modified polylinker has the
                     following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--
                     GGCCGCCTCGGCCCACGGATCC3'where n=3-4 G nucleotides.
                     WARNING: the library contains a small percentage of cDNAs
                     derived from the human host cells. Library materials
                     provided by David Sibley, Washington University."
ORIGIN

Alignment Scores:
Pred. No.:                1.16e-60        Length:          592
Score:                    652.00          Matches:         123
Percent Similarity:       97.64%          Conservative:    1
Best Local Similarity:    96.85%          Mismatches:      3
Query Match:              85.23%          Indels:          0
DB:                       7               Gaps:            0

US-10-723-083-2 (1-142) x CF370966 (1-592)

Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 145

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||:::   |||
Db        146 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGATATAGTA 205

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 265

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              |||||||||||||||||||||||||    ||||||||||||||||||||||||||||||
Db        266 CTGTACAAGCAGGGCCTGCGGGGCAGCCCCACCAAGCTCAAGGGCCCCTTGACCATGATG 325

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGACT 385

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 445

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
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Db        446 TGCTGGGAGCCAGTCCAGGAG 466

RESULT 10
BF938995
LOCUS       BF938995                565 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  7r03f11.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3706893 3'
            similar to SW:CSF2_HUMAN P04141 GRANULOCYTE-MACROPHAGE
            COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA sequence.
ACCESSION   BF938995
VERSION     BF938995.1  GI:12356315
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 565)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 497.
FEATURES             Location/Qualifiers
     source          1. .565
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3706893"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu24"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Plasmid DNA from the normalized
                     library NCI_CGAP_Lu5 was prepared, and ss circles were
                     made in vitro. Following HAP purification, this DNA was
                     used as tracer in a subtractive hybridization reaction.
                     The driver was PCR-amplified cDNAs from a pool of 5,000
                     clones made from the same library (cloneIDs
                     1414920-1417991 and 1520904-1522439). Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
ORIGIN

Alignment Scores:
Pred. No.:                3.83e-60        Length:          565
Score:                    647.00          Matches:         127
Percent Similarity:       98.45%          Conservative:    0
Best Local Similarity:    98.45%          Mismatches:      0
Query Match:              84.58%          Indels:          2
DB:                       2               Gaps:            0

US-10-723-083-2 (1-142) x BF938995 (1-565)

Qy         16 AlaProAlaArgSerProSerProSerThrGln-ProTrpGluHisValAsnAlaIle-G 35
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||| |
Db         92 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCGTGGGAGCATGTGAATGCCATCAC 151

Qy         35 lnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrV 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        152 AGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAG 211

Qy         55 alGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuG 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        212 TAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGG 271
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Qy         75 luLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetM 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        272 AGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGA 331

Qy         95 etAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnI 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 TGGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGA 391

Qy        115 leIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        392 TTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTG 451

Qy        135 spCysTrpGluProValGlnGlu 142
              |||||||||||||||||||||||
Db        452 ACTGCTGGGAGCCAGTCCAGGAG 474
```

RESULT 11
CF370833

LOCUS	CF370833 585 bp mRNA linear EST 27-AUG-2003
DEFINITION	TgESTzyj55e12.y1 Tg CAST Tachyzoite cDNA Library Toxoplasma gondii cDNA clone TgESTzyj55e12.y1 5' similar to SW:CSF2_HUMAN P04141 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR PRECURSOR ;, mRNA sequence.
ACCESSION	CF370833
VERSION	CF370833.1 GI:34318079
KEYWORDS	EST.
SOURCE	Toxoplasma gondii
ORGANISM	Toxoplasma gondii Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae; Toxoplasma.
REFERENCE	1 (bases 1 to 585)
AUTHORS	Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajioka,J.A., White,M., Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C., Tsagareishvili,R., Ronko,I., Kennedy,S., Maguire,L., Waterston,R. and Wilson,R.
TITLE	Toxoplasma EST Project
JOURNAL	Unpublished (2001)
COMMENT	Contact: Clifton, S. Toxoplasma EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: toxo@watson.wustl.edu Contact David Sibley (toxoest@borcim.wustl.edu) for further information relating to organism, libraries, or clone availability. Seq primer: -40UP from Gibco.

FEATURES Location/Qualifiers

source 1. .585
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="TgESTzyj55e12.y1"
/dev_stage="Tachyzoite"
/lab_host="ElectroTen Blue cells (Stratagene)"
/clone_lib="Tg CAST Tachyzoite cDNA Library"
/note="Vector: Modified pBluescript (pBS SK+); Site_1: BamH1; Site_2: EcoR1; The cDNA library was constructed by Keliang Tang, and Robert Cole at Washington University. cDNA was synthesized from poly(A)+ mRNA using the template-switching PCR method (SMART cDNA Kit, BD Biosciences). First strand cDNA was reverse transcribed using the CDS III/3' primer and a 5' template switch primer (Smart IV primer). The product of the first strand synthesis was PCR amplified using the same primer set and the fragments were digested with SfiI. The fragments were size selected, ligated into a modified pBluescript vector (obtained from Michael White, Montana State University) containing directional SfiI sites, and electroporated into ElectroTen Blue cells. Vector: SfiI sites were added to the multiple cloning region of pBluescript SK+ between the BamHI/EcoRI sites. The modified polylinker has the following sequence: 5'GAATTCGGCCATTACGGCC(G)n-- insert--GGCCGCCTCGGCCCACGGATCC3'where n=3-4 G nucleotides. WARNING: the library contains a small percentage of cDNAs derived from the human host cells. Library materials provided by David Sibley, Washington University."

ORIGIN

Alignment Scores:

Pred. No.:	4.01e-60	Length:	585
Score:	647.00	Matches:	123
Percent Similarity:	96.85%	Conservative:	0
Best Local Similarity:	96.85%	Mismatches:	4
Query Match:	84.58%	Indels:	0
DB:	7	Gaps:	0

US-10-723-083-2 (1-142) x CF370833 (1-585)

```
Qy         16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         86 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAG 145

Qy         36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
              ||||||||||||||||||||||||||||||||||||||||||||||||||||      |||
Db        146 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATTTAATAGTA 205

Qy         56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        206 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 265

Qy         76 LeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMet 95
              |||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        266 CTGTACAAGCAGGGCCTGCGGGGCAGCCCCACCAAGCTCAAGGGCCCCTTGACCATGATG 325

Qy         96 AlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIle 115
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        326 GCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGACT 385

Qy        116 IleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAsp 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        386 ATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGAC 445

Qy        136 CysTrpGluProValGlnGlu 142
              |||||||||||||||||||||
Db        446 TGCTGGGAGCCAGTCCAGGAG 466
```

RESULT 12
CD369973/c

LOCUS	CD369973 718 bp mRNA linear EST 05-AUG-2004
DEFINITION	UI-H-FT1-bke-o-08-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone UI-H-FT1-bke-o-08-0-UI 3', mRNA sequence.
ACCESSION	CD369973
VERSION	CD369973.1 GI:31154063
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 718)
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Gary W. Hunninghake, U of I cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/cgap.html The following repetitive elements were found in this cDNA sequence: 65-134, >(TAAA)n#Simple_repeat

```
          Seq primer: M13 FORWARD
          POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .718
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bke-o-08-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                     moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                     vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                     (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                     3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                     3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                     hours; wt adenovirus + LPS 24 hours. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT1
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

Alignment Scores:
Pred. No.:              3.06e-59        Length:         718
Score:                  640.00          Matches:        125
Percent Similarity:     99.21%          Conservative:   0
Best Local Similarity:  99.21%          Mismatches:     1
Query Match:            83.66%          Indels:         1
DB:                     6               Gaps:           0

US-10-723-083-2 (1-142) x CD369973 (1-718)

Qy         17 ProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGlnGlu 36
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        716 CCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGCCATCCAGGAG 657

Qy         37 AlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGlu 56
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        656 GCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAA 597

Qy         57 ValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeu 76
              |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        596 GTCATCTCAGAAATGTT-GACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTG 538

Qy         77 TyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAla 96
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        537 TACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCC 478

Qy         97 SerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIleIle 116
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        477 AGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATC 418

Qy        117 ThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAspCys 136
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 ACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGC 358

Qy        137 TrpGluProValGlnGlu 142
              ||||||||||||||||||
Db        357 TGGGAGCCAGTCCAGGAG 340

RESULT 13
BU633411/c
LOCUS       BU633411                701 bp    mRNA    linear   EST 23-SEP-2002
DEFINITION  UI-H-FL1-bgu-l-15-0-UI.s1 NCI_CGAP_FL1 Homo sapiens cDNA clone
            UI-H-FL1-bgu-l-15-0-UI 3', mRNA sequence.
ACCESSION   BU633411
VERSION     BU633411.1  GI:23300666
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: James Martin
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-46, >AT_rich#Low_complexity 60-129,
            >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .701
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FL1-bgu-l-15-0-UI"
                     /tissue_type="Cell lines"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FL1"
                     /note="Organ: Chondrosarcoma; Vector: pT7T3-Pac
                     (Pharmacia) with a modified polylinker; Site_1: EcoR I;
                     Site_2: Not I; NCI_CGAP_FL1 is a normalized cDNA library
                     derived from a pool of mRNA obtained from 4 cell lines
                     from grade III chondrosarcoma tissues. The library was
                     constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dT primer containing a
                     Not I site.  Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into pT7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GAGGTCGGTG. The cell lines were provided by Dr. James
                     Martin from the University of Iowa.
                     TAG_TISSUE=Human Chondrosarcoma Grade 3 cell line mix
                     TAG_LIB=UI-H-FL1
                     TAG_SEQ=GAGGTCGGTG"
ORIGIN
```

```
Alignment Scores:
Pred. No.:                2.02e-56        Length:         701
Score:                    614.00          Matches:        120
Percent Similarity:       98.36%          Conservative:   0
Best Local Similarity:    98.36%          Mismatches:     2
Query Match:              80.26%          Indels:         1
DB:                       5               Gaps:           0

US-10-723-083-2 (1-142) x BU633411 (1-701)

Qy         21 ProSerProSerThrGlnProTrpGluHisValAsnAlaIleGlnGluAlaArgArgLeu 40
              ||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        699 CCCAGCCCCAGCACGCAGCCGTGGGAGCATGTGAATCC-ATCCAGGAGGCCCGGCGTCTC 641

Qy         41 LeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrValGluValIleSerGlu 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        640 CTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTAGAAGTCATCTCAGAA 581

Qy         61 MetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGluLeuTyrLysGlnGly 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAGCTGTACAAGCAGGGC 521

Qy         81 LeuArgGlySerLeuThrLysLeuLysGlyProLeuThrMetMetAlaSerHisTyrLys 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 CTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACCATGATGGCCAGCCACTACAAG 461

Qy        101 GlnHisCysProProThrProGluThrSerCysAlaThrGlnIleIleThrPheGluSer 120
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 CAGCAGTGCCCTCCAACCCCGGAAACTTCCTGTGCAACCCAGATTATCACCTTTGAAAGT 401

Qy        121 PheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAspCysTrpGluProVal 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCCTTTGACTGCTGGGAGCCAGTC 341

Qy        141 GlnGlu 142
              ||||||
Db        340 CAGGAG 335

RESULT 14
CA307828/c
LOCUS       CA307828                 666 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  UI-H-FT1-bhx-f-10-0-UI.s1 NCI_CGAP_FT1 Homo sapiens cDNA clone
            UI-H-FT1-bhx-f-10-0-UI 3', mRNA sequence.
ACCESSION   CA307828
VERSION     CA307828.1  GI:24470882
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Gary W. Hunninghake, U of I
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
             The following repetitive elements were found in this cDNA
            sequence: 1-50, >AT_rich#Low_complexity 64-133,
            >(TAAA)n#Simple_repeat
            Seq primer: M13 FORWARD
            POLYA=Yes.
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="UI-H-FT1-bhx-f-10-0-UI"
                     /tissue_type="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI_CGAP_FT1"
                     /note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
                     modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI_CGAP_FT1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                     moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                     vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                     (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                     3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                     3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                     hours; wt adenovirus + LPS 24 hours. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT7T3-Pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dT)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG_TISSUE=Human Lung Alveolar Macrophage
                     TAG_LIB=UI-H-FT1
                     TAG_SEQ=GGCCATGCCG"
ORIGIN

Alignment Scores:
Pred. No.:                6.88e-51        Length:         666
Score:                    563.00          Matches:        108
Percent Similarity:       99.08%          Conservative:   0
Best Local Similarity:    99.08%          Mismatches:     1
Query Match:              73.59%          Indels:         0
DB:                       6               Gaps:           0

US-10-723-083-2 (1-142) x CA307828 (1-666)

Qy         34 IleGlnGluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGlu 53
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        665 ATCCAGGAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAA 606

Qy         54 ThrValGluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArg 73
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        605 ACAGTAGAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGC 546

Qy         74 LeuGluLeuTyrLysGlnGlyLeuArgGlySerLeuThrLysLeuLysGlyProLeuThr 93
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        545 TTGGAGCTGTACAAGCAGGGCCTGCGGGGCAGCCTCACCAAGCTCAAGGGCCCCTTGACC 486

Qy         94 MetMetAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThr 113
              ||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        485 ATGATGGCCAGCCANTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTGTGCAACC 426

Qy        114 GlnIleIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIlePro 133
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        425 CAGATTATCACCTTTGAAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCCC 366

Qy        134 PheAspCysTrpGluProValGlnGlu 142
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                  ||||||||||||||||||||||||||||
Db        365 TTTGACTGCTGGGAGCCAGTCCAGGAG 339

RESULT 15
AA995402
LOCUS       AA995402                475 bp    mRNA    linear   EST 27-AUG-1998
DEFINITION  or74f05.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1601601 3'
            similar to gb:M11220 GRANULOCYTE-MACROPHAGE COLONY-STIMULATING
            FACTOR PRECURSOR (HUMAN);, mRNA sequence.
ACCESSION   AA995402
VERSION     AA995402.1  GI:3181891
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 747   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 308.
FEATURES             Location/Qualifiers
     source          1. .475
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1601601"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu5"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

Alignment Scores:
Pred. No.:              1.2e-50        Length:         475
Score:                  559.00         Matches:        119
Percent Similarity:     94.49%         Conservative:   1
Best Local Similarity:  93.70%         Mismatches:     6
Query Match:            73.07%         Indels:         3
DB:                     1              Gaps:           0

US-10-723-083-2 (1-142) x AA995402 (1-475)

Qy          16 AlaProAlaArgSerProSerProSerThrGlnProTrpGluHisValAsnAlaIleGln 35
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db          55 GCACCCGCCCGCTCGCCCAGCCCCAGCACGCAGCCCTGGGAGCATGTGAATGC-ATCCAG 113

Qy          36 GluAlaArgArgLeuLeuAsnLeuSerArgAspThrAlaAlaGluMetAsnGluThrVal 55
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         114 GAGGCCCGGCGTCTCCTGAACCTGAGTAGAGACACTGCTGCTGAGATGAATGAAACAGTA 173

Qy          56 GluValIleSerGluMetPheAspLeuGlnGluProThrCysLeuGlnThrArgLeuGlu 75
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db         174 GAAGTCATCTCAGAAATGTTTGACCTCCAGGAGCCGACCTGCCTACAGACCCGCCTGGAG 233

Qy          76 LeuTyrLysGlnGlyLeuArgGlySer-LeuThrLysLeuLysGlyProLeuThrMetMe 95
               |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         234 CTGTACAAGCAGGGCCTGCGTGGCAGTCCTCACCAAGCTCAAGGGCCCCTTGACCATGAT 293

Qy          95 tAlaSerHisTyrLysGlnHisCysProProThrProGluThrSerCysAlaThrGlnIl 115
               ||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||||
Db         294 GGCCAGCCACTACAAGCAGCACTGCCCTCCAACCCCGGAAACTTCCTTTGCAAC-CAGAT 352

Qy         115 eIleThrPheGluSerPheLysGluAsnLeuLysAspPheLeuLeuValIleProPheAs 135
               |||||||      ||||||||||||||||||||||||||||||||||||||||||    |||||
Db         353 TATCACCTCTTGAAGTTTCAAAGAGAACCTGAAGGACTTTCTGCTTGTCATCCACTTTGA 412

Qy         135 pCysTrpGluProValGln 141
               ||||||||||||||:::
Db         413 CTGCTGGGAGCCAGTCAGG 431


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